183386

STIC-Biotech/ChemLib

From: Mertz, Prema
Sent: Monday, March 27, 2006 4:08 PM
To: STIC-Biotech/ChemLib
Subject: 10/849,979

Please search any 6 amino acids of SEQ ID NO:139 with protein databases.

Thanks.

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****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

Point of Contact:
Alexandra Waclawiw
Technical Info. Specialist
CM1 6A02 Tel: 308-4491
3-30
3-30

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 30, 2006, 09:04:17 ; Search time 188 Seconds
(without alignments)
1187.258 Million cell updates/sec

Title: US-10-849-979-139
Perfect score: 508
Sequence: 1 MDPKLGRMAASLLAVLLLLL.....NYIEGTKLFAAFFLEMAQLH 508

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 6

Total number of hits satisfying chosen parameters: 38162

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	508	100.0	508	4	AAB97262	Aab97262 Human car
2	508	100.0	508	4	AAG89122	Aag89122 Human sec
3	508	100.0	508	6	ABR47759	Abr47759 Human sec
4	508	100.0	508	6	ABR00082	Abr00082 Human gen
5	508	100.0	508	7	ADB91551	Adb91551 Human sec
6	508	100.0	508	7	ADC74152	Adc74152 Human sec
7	508	100.0	508	7	ADE11767	Ade11767 Human sec
8	508	100.0	509	3	AAY76144	Aay76144 Human sec
9	492	96.9	507	5	AAU72908	Aau72908 Human met
10	492	96.9	507	5	ABB07950	Abb07950 Human met
11	492	96.9	507	6	ABU69115	Abu69115 Human PRO
12	492	96.9	507	6	ABO19431	Abo19431 Human sec
13	492	96.9	507	6	ABU69092	Abu69092 Human PRO
14	492	96.9	507	6	ABU81556	Abu81556 Human sec
15	492	96.9	507	6	ADA76582	Ada76582 Novel hum
16	492	96.9	507	7	ABO25139	Abo25139 Human sec
17	492	96.9	507	7	AAE39109	Aae39109 Human PRO
18	492	96.9	507	7	AAE39046	Aae39046 Human PRO
19	492	96.9	507	7	ADC29813	Adc29813 Novel hum
20	492	96.9	507	8	ADF09256	Adf09256 Human sec
21	492	96.9	507	9	ADW12488	Adw12488 Human PRO
22	492	96.9	507	9	AEB45360	Aeb45360 Human wil
23	429	84.4	501	4	AAU28396	Aau28396 Amino aci
24	429	84.4	501	4	AAU25426	Aau25426 Human Sch
25	429	84.4	501	4	AAU15115	Aau15115 Schizophr
26	429	84.4	501	8	ADO79056	Ado79056 Schizophr
27	391	77.0	507	3	AAB18921	Aab18921 A novel p
28	336	66.1	342	4	AAM40149	Aam40149 Human pol
29	326	64.2	358	4	AAM41935	Aam41935 Human pol
30	235	46.3	508	7	ADC77691	Adc77691 Human 550
31	178	35.0	498	4	AAU26543	Aau26543 Protein e
32	148	29.1	171	8	ADQ67596	Adq67596 Novel hum
33	126	24.8	133	4	AAM25912	Aam25912 Human pro
34	119	23.4	119	4	AAM24283	Aam24283 Human EST
35	100	19.7	316	5	ABB89681	Abb89681 Human pol
36	54	10.6	100	4	ABG01654	Abg01654 Novel hum
37	41	8.1	41	9	AEB45362	Aeb45362 Fragment
38	37	7.3	157	4	ABG01653	Abg01653 Novel hum
39	26	5.1	42	9	AEB45364	Aeb45364 Fragment
40	15	3.0	15	4	AAU28401	Aau28401 Tryptic d
41	15	3.0	15	4	AAU24970	Aau24970 Schizophr
42	15	3.0	15	4	AAU26540	Aau26540 Tryptic d
43	15	3.0	15	4	AAU15314	Aau15314 Schizophr
44	15	3.0	15	8	ADO78581	Ado78581 Schizophr
45	15	3.0	15	8	ADO79039	Ado79039 Schizophr
46	14	2.8	14	4	AAU28402	Aau28402 Peptide s
47	14	2.8	14	4	AAU25421	Aau25421 Schizophr
48	14	2.8	14	4	AAU24972	Aau24972 Schizophr
49	14	2.8	14	4	AAU26541	Aau26541 Peptide #
50	14	2.8	14	4	AAU15316	Aau15316 Schizophr
51	14	2.8	14	8	ADO78583	Ado78583 Schizophr
52	14	2.8	14	8	ADO79047	Ado79047 Schizophr
53	14	2.8	20	9	AEB45366	Aeb45366 Fragment
54	11	2.2	11	4	AAU24977	Aau24977 Schizophr
55	11	2.2	11	4	AAU24971	Aau24971 Schizophr
56	11	2.2	11	4	AAU24973	Aau24973 Schizophr
57	11	2.2	11	4	AAU15321	Aau15321 Schizophr
58	11	2.2	11	4	AAU15315	Aau15315 Schizophr
59	11	2.2	11	4	AAU15317	Aau15317 Schizophr
60	11	2.2	11	8	ADO78582	Ado78582 Schizophr
61	11	2.2	11	8	ADO78584	Ado78584 Schizophr
62	11	2.2	11	8	ADO78588	Ado78588 Schizophr
63	11	2.2	415	4	ABB66250	Abb66250 Drosophil
64	11	2.2	462	4	ABB66252	Abb66252 Drosophil
65	10	2.0	10	4	AAU28403	Aau28403 Peptide s
66	10	2.0	10	4	AAU24974	Aau24974 Schizophr
67	10	2.0	10	4	AAU25422	Aau25422 Schizophr
68	10	2.0	10	4	AAU26542	Aau26542 Peptide #
69	10	2.0	10	4	AAU15318	Aau15318 Schizophr
70	10	2.0	10	8	ADO78585	Ado78585 Schizophr
71	10	2.0	10	8	ADO79049	Ado79049 Schizophr
72	10	2.0	308	8	ADY09067	Ady09067 Plant ful
73	10	2.0	318	2	AAY08759	Aay08759 L. monocy
74	10	2.0	351	7	ADM25522	Adm25522 Hyperther
75	10	2.0	379	5	ABB47976	Abb47976 Listeria
76	10	2.0	481	6	ABR52953	Abr52953 Protein s
77	10	2.0	481	7	ADK62620	Adk62620 Disease t
78	9	1.8	9	4	AAU24975	Aau24975 Schizophr
79	9	1.8	9	4	AAU15319	Aau15319 Schizophr
80	9	1.8	9	8	ADO78586	Ado78586 Schizophr
81	9	1.8	150	4	ABG03794	Abg03794 Novel hum
82	9	1.8	150	6	ABO00646	Abo00646 Novel hum
83	9	1.8	150	6	ABO00886	Abo00886 Polypepti
84	9	1.8	170	4	AAB93515	Aab93515 Human pro
85	9	1.8	194	5	AAU83607	Aau83607 Human PRO
86	9	1.8	194	5	ADY31772	Ady31772 Novel hum
87	9	1.8	194	6	ABU80754	Abu80754 Human PRO
88	9	1.8	194	6	ABO33720	Abo33720 Novel hum
89	9	1.8	194	6	ABU82063	Abu82063 Novel hum
90	9	1.8	194	6	ABJ72243	Abj72243 Human PRO
91	9	1.8	194	6	ABJ72371	Abj72371 Human PRO
92	9	1.8	194	6	ABO34266	Abo34266 Human sec
93	9	1.8	194	7	ABJ72073	Abj72073 Human mem
94	9	1.8	194	7	ADB83522	Adb83522 Novel hum
95	9	1.8	194	7	ADB80628	Adb80628 Novel hum
96	9	1.8	194	7	ADB73169	Adb73169 Novel hum
97	9	1.8	194	7	ADB78251	Adb78251 Novel hum

98	9	1.8	194	7	ADB84899	Adb84899 Human PRO
99	9	1.8	194	7	ADB78005	Adb78005 Novel hum
100	9	1.8	194	7	ADB87071	Adb87071 Human PRO
101	9	1.8	194	7	ADB84653	Adb84653 Human PRO
102	9	1.8	194	7	ADB83768	Adb83768 Novel hum
103	9	1.8	194	7	ADB72923	Adb72923 Novel hum
104	9	1.8	194	7	ADC36761	Adc36761 Human PRO
105	9	1.8	194	7	ADC21751	Adc21751 Human PRO
106	9	1.8	194	7	ADC49782	Adc49782 Novel hum
107	9	1.8	194	7	ADC48981	Adc48981 Novel hum
108	9	1.8	194	7	ADC49498	Adc49498 Novel hum
109	9	1.8	194	7	ADC47359	Adc47359 Novel hum
110	9	1.8	194	7	ADC47104	Adc47104 Novel hum
111	9	1.8	194	7	ADC77979	Adc77979 Novel hum
112	9	1.8	194	7	ADD06214	Add06214 Novel hum
113	9	1.8	194	7	ADC77733	Adc77733 Novel hum
114	9	1.8	194	7	ADD50696	Add50696 Novel hum
115	9	1.8	194	7	ADD50942	Add50942 Novel hum
116	9	1.8	194	7	ADD50423	Add50423 Human PRO
117	9	1.8	194	7	ADD50177	Add50177 Human PRO
118	9	1.8	194	7	ADD51188	Add51188 Novel hum
119	9	1.8	194	8	ADC48735	Adc48735 Novel hum
120	9	1.8	194	8	ADE20906	Ade20906 Novel hum
121	9	1.8	194	8	ADE05750	Ade05750 Human PRO
122	9	1.8	194	8	ADD74979	Add74979 Human PRO
123	9	1.8	194	8	ADD75725	Add75725 Novel hum
124	9	1.8	194	8	ADD84957	Add84957 Novel hum
125	9	1.8	194	8	ADD86783	Add86783 Novel hum
126	9	1.8	194	8	ADE20660	Ade20660 Novel hum
127	9	1.8	194	8	ADE38957	Ade38957 Novel hum
128	9	1.8	194	8	ADE05504	Ade05504 Human PRO
129	9	1.8	194	8	ADD73489	Add73489 Human PRO
130	9	1.8	194	8	ADD78329	Add78329 Novel hum
131	9	1.8	194	8	ADE21152	Ade21152 Novel hum
132	9	1.8	194	8	ADD77267	Add77267 Novel hum
133	9	1.8	194	8	ADE20414	Ade20414 Novel hum
134	9	1.8	194	8	ADD75479	Add75479 Human PRO
135	9	1.8	194	8	ADD73995	Add73995 Human PRO
136	9	1.8	194	8	ADD74241	Add74241 Human PRO
137	9	1.8	194	8	ADD75971	Add75971 Novel hum
138	9	1.8	194	8	ADD85463	Add85463 Novel hum
139	9	1.8	194	8	ADE05012	Ade05012 Human PRO
140	9	1.8	194	8	ADD75225	Add75225 Human PRO
141	9	1.8	194	8	ADD76769	Add76769 Novel hum
142	9	1.8	194	8	ADD86537	Add86537 Novel hum
143	9	1.8	194	8	ADD78005	Add78005 Novel hum
144	9	1.8	194	8	ADD77513	Add77513 Novel hum
145	9	1.8	194	8	ADD77759	Add77759 Novel hum
146	9	1.8	194	8	ADD85217	Add85217 Novel hum
147	9	1.8	194	8	ADD73749	Add73749 Human PRO
148	9	1.8	194	8	ADD74487	Add74487 Human PRO
149	9	1.8	194	8	ADD77015	Add77015 Novel hum
150	9	1.8	194	8	ADD85709	Add85709 Novel hum

ALIGNMENTS

RESULT 1
AAB97262
ID AAB97262 standard; protein; 508 AA.
XX
AC AAB97262;
XX
DT 08-AUG-2001 (first entry)
XX
DE Human carnosinase.
XX
KW Human; carnosinase; carnosine; anserine; hydrolysis; brain; epilepsy;
KW Alzheimer's disease; cognitive disorder; development abnormality;
KW foetal deficiency; neurodegenerative disorder; schizophrenia;
KW amyotrophic lateral sclerosis; Parkinson's disease; ischaemic shock.
XX
OS Homo sapiens.
XX
PN EP1097997-A1.
XX
PD 09-MAY-2001.
XX
PF 03-NOV-1999; 99EP-00402723.
XX
PR 03-NOV-1999; 99EP-00402723.
XX
PA (SNFI) SANOFI-SYNTHELABO.
XX
PI Saudek V, Smirnova-Robert T, Teufel M;
XX
DR WPI; 2001-319238/34.
DR N-PSDB; AAF27154.
XX
PT Novel isolated human carnosinase polypeptide useful for prevention and/or
PT treatment of Alzheimer's disease, amyotrophic lateral sclerosis,
PT Parkinson's disease, schizophrenia, ischemic shock, and epilepsy.
XX
PS Claim 6; Page 19-20; 27pp; English.
XX
CC The present sequence represents human carnosinase. Carnosinase is a
CC glycoprotein with an isoelectric point of 4.4. The active enzyme is a
CC dimer, with the two subunits being connected by at least one disulphide
CC bond. The enzyme is especially active in hydrolysing carnosine and
CC anserine. Carnosinase is found in high concentration in the brain.
CC Homocarnosine is hydrolysed in the brain, and carnosine and anserine are
CC split in the blood stream by carnosinase. Carnosine and anserine are
CC thought to act as cytosol buffering agents. Carnosinase its agonists and
CC antagonists and compositions containing them are useful for the
CC prevention and/or treatment of Alzheimer's disease and cognitive
CC disorders, development abnormalities and foetal deficiencies,
CC neurodegenerative disorders such as amyotrophic lateral sclerosis,
CC Parkinson's disease, schizophrenia, abnormal mental states, ischaemic
CC shock, and epilepsy
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 508; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
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Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
                ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 2
AAG89122
ID   AAG89122 standard; protein; 508 AA.
XX
AC   AAG89122;
XX
DT   11-SEP-2001  (first entry)
XX
DE   Human secreted protein, SEQ ID NO: 242.
XX
KW   Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW   GENSET.
XX
OS   Homo sapiens.
XX
PN   WO200142451-A2.
XX
PD   14-JUN-2001.
XX
PF   07-DEC-2000; 2000WO-IB001938.
XX
PR   08-DEC-1999;   99US-0169629P.
PR   06-MAR-2000; 2000US-0187470P.
XX
PA   (GEST ) GENSET.
XX
PI   Dumas Milne Edwards J,  Bougueleret L,  Jobert S;
XX
DR   WPI; 2001-367870/38.
DR   N-PSDB; AAH64725.
XX
PT   Full length GENSET human nucleic acids encoding potentially secreted
PT   proteins, useful in gene therapy and vaccination against a variety of
PT   diseases, and for diagnosis of those diseases.
XX
PS   Claim 21; Page 791-792; 921pp; English.
XX
CC   The invention relates to full length GENSET human nucleic acids encoding
CC   potentially secreted proteins. The nucleic acids and the polypeptides
CC   they encode may be used in the prevention, treatment and diagnosis of
CC   diseases associated with inappropriate GENSET gene expression. For
CC   example, they be used to treat disorders associated with decreased GENSET
CC   gene expression by rectifying mutations or deletions in a patient's
CC   genome that affect the activity of GENSET or by supplementing the
CC   patients own production of GENSET polypeptides. Conversely, antisense
CC   nucleic acid molecules may be administered to down regulate GENSET
CC   expression by binding with the cells' own genes and preventing their
CC   expression. The sense and antisense nucleic acids may also be used as DNA
CC   probes in diagnostic assays to detect and quantitate the presence of
CC   similar nucleic acid sequences in samples, and hence to determine which
CC   patients may be in need of restorative therapy. The GENSET polypeptides
CC   may be used as antigens in the production of antibodies and in assays to
CC   identify modulators (agonists and antagonists) of GENSET polypeptide
CC   expression and activity. The present sequence is a GENSET polypeptide of
CC   the invention
XX
SQ   Sequence 508 AA;

  Query Match           100.0%;  Score 508;  DB 4;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 3
ABR47759
ID   ABR47759 standard; protein; 508 AA.
XX
AC   ABR47759;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human secreted protein, SEQ ID 650.
XX
KW   Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;
KW   vulnerary; antiinflammatory; nootropic; neuroprotective;
KW   antiparkinsonian; gene therapy; human; cardiovascular disorder.
XX
OS   Homo sapiens.
XX
PN   WO200295010-A2.
XX
PD   28-NOV-2002.
XX
PF   19-MAR-2002; 2002WO-US009785.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2003-129429/12.
XX
PT   Novel human secreted proteins, useful for detecting, preventing,
PT   diagnosing, prognosticating, treating and/or ameliorating cardiovascular
PT   disorders such as arrhythmia.
XX
PS   Claim 13; SEQ ID NO 650; 1881pp; English.
XX
CC   The present invention relates to novel human secreted proteins (ABR47633-
```

```
CC   ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins
CC   and their coding sequences are useful for the preparation of a diagnostic
CC   or pharmaceutical composition for diagnosing or treating a cardiovascular
CC   disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary
CC   arteriosclerosis and myocardial ischaemia), neural disorders, immune
CC   system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, pulmonary disorders, renal disorders,
CC   proliferative disorders and/or cancerous diseases and conditions, for
CC   wound healing and epithelial cell proliferation, to treat inflammation or
CC   infection, for treating thrombosis and arteriosclerosis, for treating or
CC   preventing neural damage which occurs in neuronal disorders or
CC   neurodegenerative conditions such as Alzheimer's disease and Parkinson's
CC   disease, to enhance bone and periodontal regeneration and aid in tissue
CC   transplants or bone grafts, to prevent skin aging or hair loss, to
CC   stimulate growth and differentiation of haematopoietic cells and bone
CC   marrow cells when used in combination with other cytokines, to maintain
CC   organs before transplantation or for supporting cell culture of primary
CC   tissues, to increase or decrease differentiation or proliferation of
CC   embryonic stem cells, or to modulate mammalian characteristics or
CC   metabolism. Note: The sequence data for this patent was published in
CC   electronic format and is available from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 508;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 4
ABR00082
ID   ABR00082 standard; protein; 508 AA.
XX
AC   ABR00082;
XX
DT   03-APR-2003  (first entry)
XX
DE   Human gene 72 encoded secreted protein HHPEN62, SEQ ID NO:371.
XX
KW   Human; secreted protein; digestive disorder; gastrointestinal disorder;
KW   mouth; oesophagus; stomach; small intestine; large intestine; liver;
KW   biliary tract; pancreas; cancer; tumour; hyperproliferative disorder;
KW   immune disorder; inflammation; infection; wound healing; drug screening;
KW   chromosome identification; chromosome mapping; cytostatic;
KW   antiinflammatory; immunosuppressive; vulnerary; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200276488-A1.
XX
PD   03-OCT-2002.
XX
PF   19-MAR-2002; 2002WO-US008276.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2003-029900/02.
DR   N-PSDB; ABZ71261.
XX
PT   New human secreted proteins and nucleic acids, useful for detecting,
PT   preventing, diagnosing, prognosticating, treating and/or ameliorating
PT   e.g. gastrointestinal diseases and disorders, or cancers.
XX
PS   Claim 13; Page 984-986; 1216pp; English.
XX
CC   ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted
CC   protein genes, and ABP00011-ABP00299 represent the proteins they encode.
CC   ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The
CC   invention also encompasses antibodies specific for the secreted proteins,
CC   the use of the secreted proteins in drug screening, and recombinant
CC   vectors and host cells comprising a nucleic acid of the invention. The
CC   secreted proteins, nucleic acids encoding them, antibodies or antibody
CC   fragments specific for the secreted proteins, and modulators of protein
CC   activity are useful for diagnosing, treating, ameliorating or preventing
CC   digestive disorders. Such conditions include disorders of the mouth,
CC   oesophagus, stomach, small intestine, large intestine, liver, biliary
CC   tract and pancreas, and include cancers of these organs and tissues. The
CC   secreted proteins and their nucleic acids may also be used in the
CC   treatment of immune disorders, inflammation, infection,
CC   hyperproliferative disorders, and to promote wound healing. Nucleic acids
CC   of the invention may be used for chromosome identification, chromosome
CC   mapping, in gene therapy, for identifying individuals from minute
CC   biological samples, as hybridisation probes, and as molecular weight
CC   markers. The present sequence represents a human secreted protein of the
CC   invention
XX
SQ   Sequence 508 AA;

  Query Match             100.0%;  Score 508;  DB 6;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
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Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
```

RESULT 5
ADB91551
ID ADB91551 standard; protein; 508 AA.
XX
AC ADB91551;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human secreted protein #SEQ ID 497.
XX
KW Secreted protein; gene therapy; antidiabetic; diabetes; human.
XX
OS Homo sapiens.
XX
PN WO2003004622-A2.
XX
PD 16-JAN-2003.
XX
PF 19-MAR-2002; 2002WO-US008124.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-229407/22.
XX
PT Nucleic acid encoding a human secreted protein is useful in diagnosing or
PT treating diabetes or conditions related to diabetes.
XX
PS Claim 3; SEQ ID NO 497; 1537pp; English.
XX
CC The invention relates to isolated nucleic acid molecules ADB91065-
CC ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449-
CC ADB91834. Also disclosed is a recombinant vector comprising a
CC polynucleotide of the invention, and a recombinant host cell comprising
CC the recombinant vector. The polypeptide of the invention is useful in
CC identifying a binding partner by contacting the polypeptide with a
CC binding partner, and determining whether the binding partner increases or
CC decreases activity of the polypeptide. The polypeptide, polynucleotide,
CC antibody or its fragment, agonist or antagonist are useful for preparing
CC a pharmaceutical composition for diagnosing or treating diabetes or
CC conditions related to diabetes. The present sequence is that of the human
CC immunoglobulin Fc portion used to generate fusion proteins, increasing
CC the stability of the fused protein as compared to the secreted protein
CC only. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 508 AA;

```
  Query Match             100.0%;  Score 508;  DB 7;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
```

RESULT 6
ADC74152
ID ADC74152 standard; protein; 508 AA.
XX
AC ADC74152;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted protein - SEQ ID 785.
XX
KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;
KW antidiabetic; immunosuppressive; dermatological; nephrotropic;
KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;
KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;
KW haemopoietic; haematologic; anaemia; autoimmune disorder;
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
KW human.
XX
OS Homo sapiens.
XX
PN WO2003038063-A2.
XX

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PD   08-MAY-2003.
XX
PF   19-MAR-2002; 2002WO-US008277.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2003-430516/40.
DR   N-PSDB; ADC73537.
XX
PT   New human secreted polypeptide for diagnosing, preventing or treating
PT   hematopoietic or hematologic disorders (e.g. anemia), autoimmune
PT   disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
PT   atherosclerosis).
XX
PS   Claim 16; SEQ ID NO 785; 2272pp; English.
XX
CC   The invention relates to a novel human secreted polypeptide comprising a
CC   defined sequence given in the specification. The polypeptide, nucleic
CC   acid molecule, antibody, agonist or antagonist of the invention may be
CC   useful for preparing a composition for diagnosing or treating a
CC   haemopoietic or haematologic disorder such as anaemia, autoimmune
CC   disorders such as rheumatoid arthritis, inflammation, Grave's disease,
CC   diabetes, systemic lupus erythematosus or glomerulonephritis,
CC   neurodegenerative disorders including Parkinson's disease and Alzheimer's
CC   disease, wounds and hyperproliferative disorders including
CC   atherosclerosis or cancer, as well as bacterial, viral, fungal or
CC   parasitic infections. The polypeptide may also be used during gene
CC   therapy procedures and for identifying a binding partner by contacting
CC   the polypeptide with a binding partner and determining whether the
CC   binding partner increases or decreases the activity of the polypeptide.
CC   The current sequence is that of the human secreted protein of the
CC   invention.
XX
SQ   Sequence 508 AA;

  Query Match           100.0%;  Score 508;  DB 7;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 7
ADE11767
ID   ADE11767 standard; protein; 508 AA.
XX
AC   ADE11767;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human secreted polypeptide #22.
XX
KW   Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
KW   Alzheimer's disease; human.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003100051-A1.
XX
PD   29-MAY-2003.
XX
PF   10-SEP-2001; 2001US-00948783.
XX
PR   12-MAY-1998;   98US-0085093P.
PR   12-MAY-1998;   98US-0085094P.
PR   12-MAY-1998;   98US-0085105P.
PR   12-MAY-1998;   98US-0085180P.
PR   18-MAY-1998;   98US-0085906P.
PR   18-MAY-1998;   98US-0085920P.
PR   18-MAY-1998;   98US-0085921P.
PR   18-MAY-1998;   98US-0085922P.
PR   18-MAY-1998;   98US-0085923P.
PR   18-MAY-1998;   98US-0085924P.
PR   18-MAY-1998;   98US-0085925P.
PR   18-MAY-1998;   98US-0085927P.
PR   18-MAY-1998;   98US-0085928P.
PR   06-MAY-1999;   99WO-US009847.
PR   10-NOV-1999;   99US-00437658.
PR   11-SEP-2000;  2000US-0231846P.
PR   28-JUN-2001;  2001US-00892877.
XX
PA   (RUBE/) RUBEN S M.
PA   (FLOR/) FLORENCE K A.
PA   (NIJJ/) NI J.
PA   (ROSE/) ROSEN C A.
PA   (CART/) CARTER K C.
PA   (MOOR/) MOORE P A.
PA   (OLSE/) OLSEN H S.
PA   (SHIY/) SHI Y.
PA   (YOUN/) YOUNG P E.
PA   (WEIY/) WEI Y.
PA   (BREW/) BREWER L A.
PA   (SOPP/) SOPPET D R.
PA   (LAFL/) LAFLEUR D W.
PA   (ENDR/) ENDRESS G A.
PA   (EBNE/) EBNER R.
PA   (BIRS/) BIRSE C E.
XX
PI   Ruben SM,  Florence KA,  Ni J,  Rosen CA,  Carter KC,  Moore PA;
PI   Olsen HS,  Shi Y,  Young PE,  Wei Y,  Brewer LA,  Soppet DR,  Lafleur DW;
PI   Endress GA,  Ebner R,  Birse CE;
XX
DR   WPI; 2003-801210/75.
XX
PT   New nucleic acid molecule, useful for preparing a medicament for
```

```
PT   preventing, treating or ameliorating a medical condition e.g. cancer,
PT   liver disorders or neural disorders.
XX
PS   Claim 11; SEQ ID NO 139; 453pp; English.
XX
CC   The invention relates to human secreted polypeptides and the
CC   polynucleotides encoding them. The sequences are useful for preparing
CC   medicaments for preventing, treating or ameliorating medical conditions
CC   e.g., cancer, liver disorders such as hepatitis or neural disorders such
CC   as Alzheimer's disease. This sequence represents a human secreted
CC   polypeptide of the invention.
XX
SQ   Sequence 508 AA;

  Query Match           100.0%;  Score 508;  DB 7;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 8
AAY76144
ID   AAY76144 standard; protein; 509 AA.
XX
AC   AAY76144;
XX
DT   23-MAR-2000  (first entry)
XX
DE   Human secreted protein encoded by gene 21.
XX
KW   Human; secreted protein; cancer; tumour; developmental abnormality;
KW   foetal deficiency; blood disorder; immune system disorder; inflammation;
KW   autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW   schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW   atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW   digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW   therapy; chromosome 18q22-23.
XX
OS   Homo sapiens.
XX
PN   WO9958660-A1.
XX
PD   18-NOV-1999.
XX
PF   06-MAY-1999;   99WO-US009847.
XX
PR   12-MAY-1998;   98US-0085093P.
PR   12-MAY-1998;   98US-0085094P.
PR   12-MAY-1998;   98US-0085105P.
PR   12-MAY-1998;   98US-0085180P.
PR   18-MAY-1998;   98US-0085906P.
PR   18-MAY-1998;   98US-0085920P.
PR   18-MAY-1998;   98US-0085921P.
PR   18-MAY-1998;   98US-0085922P.
PR   18-MAY-1998;   98US-0085923P.
PR   18-MAY-1998;   98US-0085924P.
PR   18-MAY-1998;   98US-0085925P.
PR   18-MAY-1998;   98US-0085927P.
PR   18-MAY-1998;   98US-0085928P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Florence K,  Ni J,  Rosen CA,  Carter KC,  Moore PA;
PI   Olsen HS,  Shi Y,  Young PE,  Wei F,  Brewer LA,  Soppet DR,  Lafleur DW;
PI   Endress GA,  Ebner R;
XX
DR   WPI; 2000-062296/05.
DR   N-PSDB; AAZ65270.
XX
PT   New isolated human genes and the secreted polypeptides they encode,
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders.
XX
PS   Claim 11; Page 373-374; 475pp; English.
XX
CC   AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC   AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human
CC   genes. The gene encoding this protein was found to be on chromosome 18q22
CC   -23. The genes and their corresponding secreted polypeptides are useful
CC   for preventing, treating or ameliorating medical conditions, e.g. by
CC   protein or gene therapy. Also pathological conditions can be diagnosed by
CC   determining the amount of the new polypeptides in a sample or by
CC   determining the presence of mutations in the new genes. Specific uses are
CC   described for each of the 97 genes, based on which tissues they are most
CC   highly expressed in, and include developing products for the diagnosis or
CC   treatment of cancer, tumours, developmental abnormalities and foetal
CC   deficiencies, blood disorders, diseases of the immune system, autoimmune
CC   diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC   schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC   atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC   digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC   also useful for identifying their binding partners. The sequences shown
CC   in AAY76224 to AAY76424 represent fragments of the secreted proteins
XX
SQ   Sequence 509 AA;

  Query Match           100.0%;  Score 508;  DB 3;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
```

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Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVPGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVPGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
```

RESULT 9
AAU72908
ID AAU72908 standard; protein; 507 AA.
XX
AC AAU72908;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human metalloprotease partial protein sequence #20.
XX
KW Human; protease; PCR primer; cytostatic; immunomodulator; cardiant;
KW vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser;
KW hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
KW anorectic; antiinflammatory; aspartyl protease; cysteine protease;
KW metalloprotease; serine protease; cancer; haematopoietic; breast; colon;
KW lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain;
KW immune-related disease; cardiovascular disease; neuronal disease;
KW migraine; sexual dysfunction; mood disorder; attention disorder;
KW cognition disorder; hypotension; hypertension; psychotic disorder;
KW dyskinesia; metabolic disorder; inflammatory disorder.
XX
OS Homo sapiens.
XX
PN WO200183782-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-US014431.
XX
PR 04-MAY-2000; 2000US-0201879P.
XX
PA (SUGE-) SUGEN INC.
XX
PI Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI Payne V;
XX
DR WPI; 2002-041502/05.
DR N-PSDB; AAS97191.
XX
PT Novel protease polypeptide useful for screening for substances that may
PT be used to treat, e.g., cancers, immune-related diseases, cardiovascular
PT disease, migraine, pain, psychotic and inflammatory disorders.
XX
PS Claim 28; Fig 2I; 232pp; English.
XX
CC The invention relates to an isolated, enriched, or purified protease
CC polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to
CC screen for substances (S) that may modulate its activity. Administering S
CC (which modulates protease activity in vitro) may be used to treat a
CC disease or disorder selected from cancers (e.g., of tissues, of blood or
CC haematopoietic origin, of the breast, colon, lung, prostrate, cervical,
CC brain, ovarian, bladder or kidney), immune-related diseases and
CC disorders, cardiovascular disease, brain or neuronal-associated diseases
CC (e.g., central or peripheral nervous system diseases, migraine, pain,
CC sexual dysfunction, mood disorders, attention disorders, cognition
CC disorders, hypotension, hypertension, psychotic disorders, neurological
CC disorders and dyskinesias), metabolic disorders and inflammatory
CC disorders. (I) may also be useful as a diagnostic tool for a disease or
CC disorder such as those above. AAU72876-AAU72910 represent human protease
CC amino acid sequences of the invention
XX
SQ Sequence 507 AA;

Query Match 96.9%; Score 492; DB 5; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507
```

RESULT 10
ABB07950
ID ABB07950 standard; protein; 507 AA.
XX
AC ABB07950;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human metalloprotease, 55054.
XX
KW 55054; human; metalloprotease; neural cell; cerebral injury; vulnerary;
KW enzyme.
XX
OS Homo sapiens.
XX
PN WO200226948-A2.

XX
PD 04-APR-2002.
XX
PF 25-SEP-2001; 2001WO-US030016.
XX
PR 25-SEP-2000; 2000US-0235055P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Kapeller-Libermann R;
XX
DR WPI; 2002-405051/43.
DR N-PSDB; ABL58476, ABL58477.
XX
PT Identifying modulator of neural cell growth or transition metal
PT neurotoxicity, involves contacting test compound with novel human
PT metalloprotease polypeptide and determining if the polypeptide binds the
PT test compound.
XX
PS Claim 21; Fig 1A-D; 105pp; English.
XX
CC The invention provides a method for identifying a modulator of neural
CC cell growth, cerebral injury or wound healing, transition metal
CC neurotoxicity, histamine production, neural/hepatic cell proliferation or
CC degradation of extracellular matrix, neurotransmitter or soluble
CC intracellular/extracellular dipeptide. The method involves contacting a
CC test compound and metalloprotease polypeptide, selected from a human
CC metalloprotease polypeptide, termed 55054, and determining if 55054 binds
CC the test compound. The metalloprotease, 55054 is useful for making a
CC pharmaceutical composition for inhibiting the ability of a cell selected
CC from a neural cell such as glial cell or neuron (a sensory neuron or
CC olfactory sensory neuron), astrocyte, oligodendrocyte and ensheathing
CC cell, to cleave a polypeptide. The present sequence represents the human
CC metalloprotease, 55054
XX
SQ Sequence 507 AA;

Query Match 96.9%; Score 492; DB 5; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495
```

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Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507
```

RESULT 11
ABU69115
ID ABU69115 standard; protein; 507 AA.
XX
AC ABU69115;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #13.
XX
KW Human; secreted and transmembrane protein; bone disorder; obesity;
KW cartilage disorder; sports injury; arthritis; diabetes mellitus;
KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassaemia;
KW haemoglobin-associated disorder; kidney disorder; Berger disease;
KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;
KW celiac disease; dermatitis herpetiformis; Crohn's disease; anorectic;
KW antiarthritic; antidiabetic; antianaemic; nephrotropic; antiinflammatory.
XX
OS Homo sapiens.
XX
PN US2003032061-A1.
XX
PD 13-FEB-2003.
XX
PF 26-DEC-2001; 2001US-00036214.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.

```
PR   09-JUL-2001; 2001WO-US021735.
PR   16-AUG-2001; 2001US-00931836.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-341962/32.
DR   N-PSDB; ACA06168.
XX
PT   Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1889, PRO1890,
PT   PRO1887, PRO1785, PRO4353, useful for treating sports injuries,
PT   arthritis, diabetes, obesity, hyper- or hypo-insulinemia.
XX
PS   Claim 12; Fig 26; 194pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides and polynucleotides are useful in diagnosing or treating
CC   various bone and/or cartilage disorders (e.g. sports injuries,
CC   arthritis), various insulin deficient states (e.g. diabetes mellitus,
CC   hypo-insulinaemia), obesity, hyper-insulinaemia, haemoglobin-associated
CC   disorders (e.g. thalassaemias), kidney disorders associated with
CC   decreased mesangial cell function (e.g. Berger disease), or other
CC   nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC   dermatitis herpetiformis or Crohn's disease. The PRO polynucleotide
CC   sequences may be used as hybridisation probes in chromosome and gene
CC   mapping, or in generating antisense RNA and DNA. They are also useful in
CC   preparing PRO polypeptides, in assays to identify other proteins or
CC   molecules involved in binding reaction, to generate transgenic animals or
CC   knockout animals, which in turn are useful in the development and
CC   screening of therapeutically useful reagents, for chromosome
CC   identification, and tissue typing. The PRO polypeptides and nucleic acid
CC   molecules are also useful in gene therapy, and as molecular weight
CC   markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC   used in diagnostic assays for PRO polypeptides, or for the affinity
CC   purification of the polypeptides from recombinant cell culture or natural
CC   sources. ABU69103-ABU69125 represent the human PRO polypeptides of the
CC   invention
XX
SQ   Sequence 507 AA;

  Query Match            96.9%;  Score 492;  DB 6;  Length 507;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 12
ABO19431
ID   ABO19431 standard; protein; 507 AA.
XX
AC   ABO19431;
XX
DT   27-AUG-2003  (first entry)
XX
DE   Human secreted / transmembrane polypeptide PRO4380.
XX
KW   Human; gene therapy; diabetes; obesity; hypoinsulinaemia.
XX
OS   Homo sapiens.
XX
PN   US2003027249-A1.
XX
PD   06-FEB-2003.
XX
PF   16-AUG-2001; 2001US-00931836.
XX
PR   15-MAY-1998;   98US-0085579P.
PR   15-DEC-1998;   98US-0112514P.
PR   22-DEC-1998;   98US-0113300P.
PR   23-DEC-1998;   98US-0113430P.
PR   23-DEC-1998;   98US-0113605P.
PR   23-DEC-1998;   98US-0113621P.
PR   23-DEC-1998;   98US-0114140P.
PR   12-JAN-1999;   99US-0115552P.
PR   22-JAN-1999;   99US-0116843P.
PR   23-MAR-1999;   99US-0125774P.
PR   23-MAR-1999;   99US-0125778P.
PR   24-MAR-1999;   99US-0125826P.
PR   31-MAR-1999;   99US-0127035P.
PR   05-APR-1999;   99US-0127706P.
PR   13-APR-1999;   99US-0129122P.
PR   21-APR-1999;   99US-0130359P.
PR   27-APR-1999;   99US-0131270P.
PR   27-APR-1999;   99US-0131272P.
PR   27-APR-1999;   99US-0131291P.
PR   04-MAY-1999;   99US-0132371P.
PR   04-MAY-1999;   99US-0132379P.
PR   04-MAY-1999;   99US-0132383P.
PR   14-MAY-1999;   99US-00311832.
PR   14-MAY-1999;   99WO-US010733.
PR   25-MAY-1999;   99US-0135750P.
PR   08-JUN-1999;   99US-0138166P.
PR   20-JUL-1999;   99US-0144791P.
PR   03-AUG-1999;   99US-0146970P.
PR   25-AUG-1999;   99US-00380142.
PR   29-OCT-1999;   99US-0162506P.
PR   02-DEC-1999;   99WO-US028551.
PR   22-DEC-1999;   99WO-US030720.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   22-AUG-2000; 2000US-00644848.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
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PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   22-MAR-2001; 2001US-00816744.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   01-JUN-2001; 2001WO-US017800.
PR   05-JUN-2001; 2001US-00874503.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001US-00869599.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   18-JUL-2001; 2001US-00908827.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-492030/46.
DR   N-PSDB; ACD28837.
XX
PT   New isolated, secreted and transmembrane PRO polypeptides and encoding
PT   nucleic acids, useful for the diagnosis and treatment of disorders such
PT   as diabetes, obesity and/or hypoinsulinemia.
XX
PS   Claim 12; Fig 26; 196pp; English.
XX
CC   The invention relates to a new isolated nucleic acid which encodes a PRO
CC   polypeptide. The methods and compositions of the present invention are
CC   useful for the diagnosis and treatment of disorders associated with the
CC   PRO polypeptides, such as diabetes, obesity and hypoinsulinaemia. The
CC   present sequence represents the amino acid sequence of a human secreted
CC   and transmembrane PRO polypeptide
XX
SQ   Sequence 507 AA;

  Query Match           96.9%;  Score 492;  DB 6;  Length 507;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 13
ABU69092
ID   ABU69092 standard; protein; 507 AA.
XX
AC   ABU69092;
XX
DT   02-JUN-2003  (first entry)
XX
DE   Human PRO polypeptide #13.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein; cancer;
KW   non-insulin dependent diabetes mellitus; septic shock; stroke;
KW   rheumatoid arthritis; graft-versus-host disease; cardiac ischaemia;
KW   psoriasis; inflammatory bowel disease; asthma; antidiabetic; cytostatic;
KW   immunosuppressive; antirheumatic; antiarthritic; cerebroprotective;
KW   vasotropic; antipsoriatic; antiinflammatory; antiasthmatic.
XX
OS   Homo sapiens.
XX
PN   US2003008348-A1.
XX
PD   09-JAN-2003.
XX
PF   26-DEC-2001; 2001US-00035855.
XX
PR   15-MAY-1998;   98US-0085579P.
PR   15-DEC-1998;   98US-0112514P.
PR   22-DEC-1998;   98US-0113300P.
PR   23-DEC-1998;   98US-0113430P.
PR   23-DEC-1998;   98US-0113605P.
PR   23-DEC-1998;   98US-0113621P.
PR   23-DEC-1998;   98US-0114140P.
PR   12-JAN-1999;   99US-0115552P.
PR   22-JAN-1999;   99US-0116843P.
PR   23-MAR-1999;   99US-0125774P.
PR   23-MAR-1999;   99US-0125778P.
PR   24-MAR-1999;   99US-0125826P.
PR   31-MAR-1999;   99US-0127035P.
PR   05-APR-1999;   99US-0127706P.
PR   13-APR-1999;   99US-0129122P.
PR   21-APR-1999;   99US-0130359P.
PR   27-APR-1999;   99US-0131270P.
PR   27-APR-1999;   99US-0131272P.
PR   27-APR-1999;   99US-0131291P.
PR   04-MAY-1999;   99US-0132371P.
PR   04-MAY-1999;   99US-0132379P.
PR   04-MAY-1999;   99US-0132383P.
PR   14-MAY-1999;   99WO-US010733.
PR   25-MAY-1999;   99US-0135750P.
PR   08-JUN-1999;   99US-0138166P.
PR   20-JUL-1999;   99US-0144791P.
PR   03-AUG-1999;   99US-0146970P.
PR   29-OCT-1999;   99US-0162506P.
PR   02-DEC-1999;   99WO-US028551.
PR   22-DEC-1999;   99WO-US030720.
PR   01-MAR-2000;  2000WO-US005601.
PR   02-MAR-2000;  2000WO-US005841.
PR   22-MAY-2000;  2000WO-US014042.
PR   02-JUN-2000;  2000WO-US015264.
PR   23-AUG-2000;  2000WO-US023522.
PR   24-AUG-2000;  2000WO-US023328.
PR   01-DEC-2000;  2000WO-US032678.
PR   20-DEC-2000;  2000WO-US034956.
PR   28-FEB-2001;  2001WO-US006520.
PR   01-JUN-2001;  2001WO-US017800.
PR   20-JUN-2001;  2001WO-US019692.
PR   29-JUN-2001;  2001WO-US021066.
PR   09-JUL-2001;  2001WO-US021735.
PR   16-AUG-2001;  2001US-00931836.
```

```
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-341326/32.
DR   N-PSDB; ACA06111.
XX
PT   New PRO polypeptides and nucleic acid molecules, useful for diagnosing or
PT   treating diabetes mellitus, cancers, septic shock, inflammatory bowel
PT   disease or asthma, or in gene therapy, chromosome identification or
PT   tissue typing.
XX
PS   Claim 12; Fig 26; 196pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides and polynucleotides are useful in diagnosing or treating non
CC   -insulin dependent diabetes mellitus, cancers, septic shock, rheumatoid
CC   arthritis, graft-versus-host disease, stroke, cardiac ischaemia,
CC   psoriasis, inflammatory bowel disease or asthma. The PRO polynucleotide
CC   sequences may be used as hybridisation probes in chromosome and gene
CC   mapping, or in generating antisense RNA and DNA. They are also useful in
CC   preparing PRO polypeptides, in assays to identify other proteins or
CC   molecules involved in binding reaction, to generate transgenic animals or
CC   knockout animals, which in turn are useful in the development and
CC   screening of therapeutically useful reagents, for chromosome
CC   identification, and tissue typing. The PRO polypeptides and nucleic acid
CC   molecules are also useful in gene therapy, and as molecular weight
CC   markers for protein electrophoresis purposes. Anti-PRO antibodies may be
CC   used in diagnostic assays for PRO polypeptides, or for the affinity
CC   purification of the polypeptides from recombinant cell culture or natural
CC   sources. ABU69080-ABU69102 represent the human PRO polypeptides of the
CC   invention
XX
SQ   Sequence 507 AA;

  Query Match             96.9%;  Score 492;  DB 6;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 14
ABU81556
ID   ABU81556 standard; protein; 507 AA.
XX
AC   ABU81556;
XX
DT   24-JUN-2003  (first entry)
XX
DE   Human secreted polypeptide PRO4380.
XX
KW   Human; inflammatory disease; organ failure; atherosclerosis; cancer;
KW   cardiac injury; infertility; birth defect; premature aging; AIDS;
KW   differentiation disorder; cell adhesin disorder; skin disorder;
KW   neural receptor disorder; diabetic complication; tissue typing.
XX
OS   Homo sapiens.
XX
PN   US2002192751-A1.
XX
PD   19-DEC-2002.
XX
PF   26-DEC-2001; 2001US-00036041.
XX
PR   15-MAY-1998;   98US-0085579P.
PR   15-DEC-1998;   98US-0112514P.
PR   22-DEC-1998;   98US-0113300P.
PR   23-DEC-1998;   98US-0113430P.
PR   23-DEC-1998;   98US-0113605P.
PR   23-DEC-1998;   98US-0113621P.
PR   23-DEC-1998;   98US-0114140P.
PR   12-JAN-1999;   99US-0115552P.
PR   22-JAN-1999;   99US-0116843P.
PR   23-MAR-1999;   99US-0125774P.
PR   23-MAR-1999;   99US-0125778P.
PR   24-MAR-1999;   99US-0125826P.
PR   31-MAR-1999;   99US-0127035P.
PR   05-APR-1999;   99US-0127706P.
PR   13-APR-1999;   99US-0129122P.
PR   21-APR-1999;   99US-0130359P.
PR   27-APR-1999;   99US-0131270P.
PR   27-APR-1999;   99US-0131272P.
PR   27-APR-1999;   99US-0131291P.
PR   04-MAY-1999;   99US-0132371P.
PR   04-MAY-1999;   99US-0132379P.
PR   04-MAY-1999;   99US-0132383P.
PR   14-MAY-1999;   99WO-US010733.
PR   25-MAY-1999;   99US-0135750P.
PR   08-JUN-1999;   99US-0138166P.
PR   20-JUL-1999;   99US-0144791P.
PR   03-AUG-1999;   99US-0146970P.
PR   29-OCT-1999;   99US-0162506P.
PR   02-DEC-1999;   99WO-US028551.
PR   22-DEC-1999;   99WO-US030720.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
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PR   16-AUG-2001; 2001US-00931836.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-341079/32.
DR   N-PSDB; ACA67734.
XX
PT   New secreted and transmembrane nucleic acids and polypeptides, designated
PT   as PRO, useful for treating inflammation, organ failure, atherosclerosis,
PT   cardiac injury, infertility, birth defects, premature aging, AIDS, or
PT   cancer.
XX
PS   Claim 12; Fig 26; 195pp; English.
XX
CC   The invention relates to an isolated nucleic acid that encodes a PRO
CC   polypeptide. The nucleic acids and polypeptides are useful for treating
CC   inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
CC   infertility, birth defects, premature aging, acquired immunodeficiency
CC   syndrome (AIDS), cancer, differentiation disorders, cell adhesin
CC   disorders, neural receptor disorders, skin disorders or diabetic
CC   complications. The nucleic acids are useful as hybridisation probes, in
CC   chromosome and gene mapping and in generating antisense RNA or DNA. The
CC   polypeptides are useful as pharmaceuticals, diagnostics, biosensors or
CC   bioreactors. Both are useful in tissue typing. The present sequence
CC   represents the amino acid sequence of a PRO polypeptide of the invention
XX
SQ   Sequence 507 AA;

  Query Match             96.9%;  Score 492;  DB 6;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 15
ADA76582
ID   ADA76582 standard; protein; 507 AA.
XX
AC   ADA76582;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO4380.
XX
KW   human; secreted and transmembrane protein; PRO; tumour; gene therapy;
KW   tissue typing; chromosome identification; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2003036114-A1.
XX
PD   20-FEB-2003.
XX
PF   26-DEC-2001; 2001US-00035719.
XX
PR   15-MAY-1998;   98US-0085579P.
PR   15-DEC-1998;   98US-0112514P.
PR   22-DEC-1998;   98US-0113300P.
PR   23-DEC-1998;   98US-0113430P.
PR   23-DEC-1998;   98US-0113605P.
PR   23-DEC-1998;   98US-0113621P.
PR   23-DEC-1998;   98US-0114140P.
PR   12-JAN-1999;   99US-0115552P.
PR   22-JAN-1999;   99US-0116843P.
PR   23-MAR-1999;   99US-0125774P.
PR   23-MAR-1999;   99US-0125778P.
PR   24-MAR-1999;   99US-0125826P.
PR   31-MAR-1999;   99US-0127035P.
PR   05-APR-1999;   99US-0127706P.
PR   13-APR-1999;   99US-0129122P.
PR   21-APR-1999;   99US-0130359P.
PR   27-APR-1999;   99US-0131270P.
PR   27-APR-1999;   99US-0131272P.
PR   27-APR-1999;   99US-0131291P.
PR   04-MAY-1999;   99US-0132371P.
PR   04-MAY-1999;   99US-0132379P.
PR   04-MAY-1999;   99US-0132383P.
PR   14-MAY-1999;   99WO-US010733.
PR   25-MAY-1999;   99US-0135750P.
PR   08-JUN-1999;   99US-0138166P.
PR   20-JUL-1999;   99US-0144791P.
PR   03-AUG-1999;   99US-0146970P.
PR   29-OCT-1999;   99US-0162506P.
PR   02-DEC-1999;   99WO-US028551.
PR   22-DEC-1999;   99WO-US030720.
PR   01-MAR-2000;  2000WO-US005601.
PR   02-MAR-2000;  2000WO-US005841.
PR   22-MAY-2000;  2000WO-US014042.
PR   02-JUN-2000;  2000WO-US015264.
PR   23-AUG-2000;  2000WO-US023522.
PR   24-AUG-2000;  2000WO-US023328.
PR   01-DEC-2000;  2000WO-US032678.
PR   20-DEC-2000;  2000WO-US034956.
PR   28-FEB-2001;  2001WO-US006520.
PR   01-JUN-2001;  2001WO-US017800.
PR   20-JUN-2001;  2001WO-US019692.
PR   29-JUN-2001;  2001WO-US021066.
PR   09-JUL-2001;  2001WO-US021735.
PR   16-AUG-2001;  2001US-00931836.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-615764/58.
DR   N-PSDB; ADA76581.
XX
```

PT Novel isolated secreted and transmembrane polypeptides, designated as PRO
PT polypeptides e.g. PRO1484, PRO4334 and PRO1122, useful for inhibiting
PT tumor cell growth, and for preparing medicaments for therapeutic use.
XX
PS Claim 12; Fig 26; 201pp; English.
XX
CC The invention describes an isolated secreted and transmembrane PRO
CC polypeptide (I), having at least 80% identity to or scoring at least 80%
CC positives when compared to, a sequence (S1) comprising 246, 440, 197, 97,
CC 273, 571, 209, 888, 502, 310, 251, 800, 507, 248, 223, 134, 136, 468,
CC 328, 221, 194, 899, or 339 amino acids fully defined in the
CC specification. An anti-(I)-antibody is useful for determining the
CC presence of (I) in a cell. (I) is useful for identifying a compound
CC capable of inhibiting the expression and/or activity of (I). (I) and the
CC antibody are useful for inhibiting the growth of tumour cells, and for
CC the preparation of a medicament useful in the treatment of a condition
CC which is responsive to (I) or the antibody. A polynucleotide (II)
CC encoding (I) is also useful for isolating full-length PRO cDNA for
CC generating transgenic animals or knock-out animals, which are, in turn,
CC are useful in the development in the screening of therapeutically useful
CC reagents, and in gene therapy. PRO is useful in assays to identify other
CC proteins or molecules involved in binding interactions, for screening
CC inhibitors or agonists of binding interactions and for screening chemical
CC libraries. (I) is useful as molecular weight marker for protein
CC electrophoresis, and as therapeutic agents. (I) or (II) is useful for
CC tissue typing and for chromosome identification. Ab is useful in
CC diagnostic assays for PRO, in affinity purification of PRO, and for
CC detection of PRO in biological samples. This is the amino acid sequence
CC of a novel human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 507 AA;

Query Match 96.9%; Score 492; DB 6; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507
```

RESULT 16
ABO25139
ID ABO25139 standard; protein; 507 AA.
XX
AC ABO25139;
XX
DT 05-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane protein PRO4380.
XX
KW Human; PRO; secreted protein; transmembrane protein; septic shock;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003044842-A1.
XX
PD 06-MAR-2003.
XX
PF 26-DEC-2001; 2001US-00036160.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-492260/46.
DR N-PSDB; ACD42296.

```
XX
PT   Novel secreted and transmembrane polypeptide for identifying agonists or
PT   antagonists of polypeptide, and as molecular weight markers.
XX
PS   Claim 12; Fig 26; 195pp; English.
XX
CC   The invention relates to an isolated, secreted and transmembrane
CC   polypeptide, termed PRO polypeptide, PRO having at least 80 % sequence
CC   identity to any one of the 23 100-900 residue amino acid sequences, given
CC   in the specification or to a sequence encoded by a nucleic acid molecule
CC   deposited under any one of the ATCC accession numbers given in the
CC   specification. Also included are an isolated nucleic acid molecule having
CC   at least 80 % sequence identity to any one of 23 400-3500 nucleotide
CC   sequences given in the specification, (or a nucleotide sequence encoding
CC   PRO, a full- length PRO coding sequence, a full-length coding sequence of
CC   DNA deposited under any ATCC accession number given in the specification)
CC   or at least 80 % identity to a nucleotide sequence encoding PRO, lacking
CC   its associated signal peptide, a sequence encoding extracellular domain
CC   of PRO with or without its associated signal peptide, a vector comprising
CC   the PRO nucleic acid, a host cell comprising the vector, preparation of
CC   PRO, a chimeric molecule comprising PRO fused to a heterologous amino
CC   acid sequence and an anti-PRO antibody. PRO is useful for identifying
CC   ant/agonists or antagonists of PRO, preparing a variant of PRO, as
CC   molecular weight markers and PRO nucleic acid is useful for recombinantly
CC   expressing those markers. PRO is also useful as therapeutic agent. PRO is
CC   useful in assays to identify molecules or proteins which bind to PRO and
CC   for identifying inhibitors of PRO. PRO nucleic acid is useful as a
CC   hybridisation probe, in chromosome and gene mapping, in generation of
CC   antisense RNA and DNA, for generating transgenic animals or knockout
CC   animals which in turn are useful in the development and screening of
CC   therapeutically useful reagents. PRO nucleic acid is also useful in
CC   mapping the gene which encodes the PRO and for the genetic analysis of
CC   individuals with genetic disorders, in gene therapy, for chromosome
CC   identification, as chromosome marker, and for generating probes for PCR,
CC   Northern analysis, Southern analysis and Western analysis. The antibody
CC   useful in diagnostic assays for PRO, for affinity purification of PRO,
CC   and for treating septic shock. PRO or the antibody is useful for the
CC   preparation of medicament for treating conditions which is responsive to
CC   the PRO polypeptide or anti-PRO antibody. PRO and PRO nucleic acid are
CC   useful for tissue typing. The present sequence represents a PRO protein
XX
SQ   Sequence 507 AA;

  Query Match             96.9%;  Score 492;  DB 7;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 17
AAE39109
ID   AAE39109 standard; protein; 507 AA.
XX
AC   AAE39109;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human PRO4380 protein.
XX
KW   Human; PRO protein; inflammation; nephropathy; bone disorder; arthritis;
KW   cartilage disorder; diabetes; gene therapy; antisense therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .26
FT                   /label= Signal_peptide
FT   Protein         27. .507
FT                   /note= "Mature human PRO protein"
FT   Modified-site   89. .95
FT                   /note= "N-myristoylation site"
FT   Modified-site   119. .125
FT                   /note= "N-myristoylation site"
FT   Binding-site    140. .143
FT                   /note= "Cell attachment site"
FT   Region          156. .167
FT                   /note= "ArgE/dapE/ACY1/CPG"
FT   Modified-site   162. .168
FT                   /note= "N-myristoylation site"
FT   Modified-site   197. .203
FT                   /note= "N-myristoylation site"
FT   Modified-site   242. .248
FT                   /note= "N-myristoylation site"
FT   Modified-site   263. .269
FT                   /note= "N-myristoylation site"
FT   Domain          273. .292
FT                   /note= "Transmembrane domain"
FT   Modified-site   322. .326
FT                   /note= "N-glycosylation site"
FT   Modified-site   351. .357
FT                   /note= "N-myristoylation site"
FT   Modified-site   382. .386
FT                   /note= "N-glycosylation site"
FT   Modified-site   400. .404
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
FT   Modified-site   402. .406
FT                   /note= "N-glycosylation site"
XX
PN   US2003049733-A1.
XX
PD   13-MAR-2003.
XX
PF   26-DEC-2001; 2001US-00035958.
XX
PR   15-MAY-1998;   98US-0085579P.
PR   15-DEC-1998;   98US-0112514P.
PR   22-DEC-1998;   98US-0113300P.
PR   23-DEC-1998;   98US-0113430P.
PR   23-DEC-1998;   98US-0113605P.
PR   23-DEC-1998;   98US-0113621P.
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PR   23-DEC-1998;   98US-0114140P.
PR   12-JAN-1999;   99US-0115552P.
PR   22-JAN-1999;   99US-0116843P.
PR   23-MAR-1999;   99US-0125774P.
PR   23-MAR-1999;   99US-0125778P.
PR   24-MAR-1999;   99US-0125826P.
PR   31-MAR-1999;   99US-0127035P.
PR   05-APR-1999;   99US-0127706P.
PR   13-APR-1999;   99US-0129122P.
PR   21-APR-1999;   99US-0130359P.
PR   27-APR-1999;   99US-0131270P.
PR   27-APR-1999;   99US-0131272P.
PR   27-APR-1999;   99US-0131291P.
PR   04-MAY-1999;   99US-0132371P.
PR   04-MAY-1999;   99US-0132379P.
PR   04-MAY-1999;   99US-0132383P.
PR   14-MAY-1999;   99WO-US010733.
PR   25-MAY-1999;   99US-0135750P.
PR   08-JUN-1999;   99US-0138166P.
PR   20-JUL-1999;   99US-0144791P.
PR   03-AUG-1999;   99US-0146970P.
PR   29-OCT-1999;   99US-0162506P.
PR   02-DEC-1999;   99WO-US028551.
PR   22-DEC-1999;   99WO-US030720.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   16-AUG-2001; 2001US-00931836.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-585109/55.
DR   N-PSDB; AAD59362.
XX
PT   New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT   acids, useful for diagnosing, preventing and/or treating inflammation,
PT   nephropathies, bone and cartilage disorders, and diabetes.
XX
PS   Claim 12; Fig 26; 203pp; English.
XX
CC   The invention relates to an isolated nucleic acid that encodes a PRO
CC   polypeptide. The methods and compositions of the present invention are
CC   useful for the diagnosis, prevention and/or treatment of inflammation,
CC   nephropathies, bone and cartilage disorders, such as arthritis and
CC   disorders that affect glucose or free fatty acid (FFA) uptake, such as
CC   diabetes, hypoinsulinaemia or hyperinsulinaemia. The PRO polypeptides are
CC   also useful as molecular weight markers or for chromosome identification.
CC   The PRO genes are useful as hybridisation probes or for screening
CC   libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be
CC   used in gene therapy and antisense therapy. The present sequence is human
CC   PRO protein
XX
SQ   Sequence 507 AA;

  Query Match             96.9%;  Score 492;  DB 7;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 18
AAE39046
ID   AAE39046 standard; protein; 507 AA.
XX
AC   AAE39046;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human PRO4380 protein.
XX
KW   Human; diagnosis; inflammation; nephropathy; bone disorder; arthritis;
KW   cartilage disorder; hypoinsulinaemia; hyperinsulinaemia; gene therapy;
KW   antisense therapy; diabetes; PRO.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1. .26
FT                    /label= Signal_peptide
FT   Protein          27. .507
FT                    /note= "Mature human PRO protein"
FT   Modified-site    89. .95
FT                    /note= "N-myristoylation site"
FT   Modified-site    119. .125
FT                    /note= "N-myristoylation site"
FT   Binding-site     140. .143
FT                    /note= "Cell attachment sequence"
FT   Region           156. .167
FT                    /note= "ArgE/dapE/ACY1/CPG"
FT   Modified-site    162. .168
FT                    /note= "N-myristoylation site"
FT   Modified-site    197. .203
FT                    /note= "N-myristoylation site"
FT   Modified-site    242. .248
FT                    /note= "N-myristoylation site"
FT   Modified-site    263. .269
FT                    /note= "N-myristoylation site"
FT   Domain           273. .292
```

```
PT                  /note= "Transmembrane domain"
FT   Modified-site  322. .326
FT                  /note= "N-glycosylation site"
FT   Modified-site  351. .357
FT                  /note= "N-myristoylation site"
FT   Modified-site  382. .386
FT                  /note= "N-glycosylation site"
FT   Modified-site  400. .404
FT                  /note= "cAMP and cGMP dependent protein kinase
FT                  phosphorylation site"
FT   Modified-site  402. .406
FT                  /note= "N-glycosylation site"
XX
PN   US2003049734-A1.
XX
PD   13-MAR-2003.
XX
PF   26-DEC-2001; 2001US-00036150.
XX
PR   15-MAY-1998;   98US-0085579P.
PR   15-DEC-1998;   98US-0112514P.
PR   22-DEC-1998;   98US-0113300P.
PR   23-DEC-1998;   98US-0113430P.
PR   23-DEC-1998;   98US-0113605P.
PR   23-DEC-1998;   98US-0113621P.
PR   23-DEC-1998;   98US-0114140P.
PR   12-JAN-1999;   99US-0115552P.
PR   22-JAN-1999;   99US-0116843P.
PR   23-MAR-1999;   99US-0125774P.
PR   23-MAR-1999;   99US-0125778P.
PR   24-MAR-1999;   99US-0125826P.
PR   31-MAR-1999;   99US-0127035P.
PR   05-APR-1999;   99US-0127706P.
PR   13-APR-1999;   99US-0129122P.
PR   21-APR-1999;   99US-0130359P.
PR   27-APR-1999;   99US-0131270P.
PR   27-APR-1999;   99US-0131272P.
PR   27-APR-1999;   99US-0131291P.
PR   04-MAY-1999;   99US-0132371P.
PR   04-MAY-1999;   99US-0132379P.
PR   04-MAY-1999;   99US-0132383P.
PR   14-MAY-1999;   99WO-US010733.
PR   25-MAY-1999;   99US-0135750P.
PR   08-JUN-1999;   99US-0138166P.
PR   20-JUL-1999;   99US-0144791P.
PR   03-AUG-1999;   99US-0146970P.
PR   29-OCT-1999;   99US-0162506P.
PR   02-DEC-1999;   99WO-US028551.
PR   22-DEC-1999;   99WO-US030720.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   22-MAY-2000; 2000WO-US014042.
PR   02-JUN-2000; 2000WO-US015264.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000WO-US034956.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   16-AUG-2001; 2001US-00931836.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-585110/55.
DR   N-PSDB; AAD59237.
XX
PT   New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT   acids, useful for diagnosing, preventing and/or treating inflammation,
PT   nephropathies, bone and cartilage disorders, and diabetes.
XX
PS   Claim 12; Fig 26; 195pp; English.
XX
CC   The present invention relates to novel polypeptides and nucleic acids
CC   encoding them. The methods and compositions of the present invention are
CC   useful for the diagnosis, prevention and/or treatment of inflammation,
CC   nephropathies, bone and cartilage disorders such as arthritis and
CC   disorders that affect glucose or free fatty acid (FFA) uptake such as
CC   diabetes, hypoinsulinaemia and hyperinsulinaemia. The PRO peptides are
CC   useful as molecular weight markers and for chromosome identification. The
CC   PRO genes may also be used in gene therapy and antisense therapy. The
CC   present sequence is human PRO protein
XX
SQ   Sequence 507 AA;

  Query Match             96.9%;  Score 492;  DB 7;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 19
ADC29813
ID   ADC29813 standard; protein; 507 AA.
XX
AC   ADC29813;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO4380.
XX
KW   human; secreted and transmembrane protein; PRO; vulnerary; antiarthritic;
KW   antidiabetic; anorectic; antianaemic; dermatological; antiinflammatory;
KW   antiallergic; immunosuppressive; gastrointestinal;
KW   chondrocyte cell differentiation; glucose uptake stimulator;
KW   pancreatic beta cell differentiation; mesangial cell proliferation;
```

KW tissue typing; chromosome identification; gene therapy;
KW chromosome mapping; gene mapping; sports injury; arthritis; diabetes;
KW obesity; hyper-insulinaemia; hypo-insulinaemia; thalassaemia;
KW Berger disease; Schonlein-Henoch purpura; celiac disease;
KW dermatitis herpetiformis; Crohn's disease.
XX
OS Homo sapiens.
XX
PN US2003092063-A1.
XX
PD 15-MAY-2003.
XX
PF 26-DEC-2001; 2001US-00036063.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-765478/72.
DR N-PSDB; ADC29812.
XX
PT Novel isolated PRO polypeptide such as PRO1484, PRO4334, PRO1122,
PT PRO1889, PRO1890, PRO1887, PRO1785, useful for treating arthritis,
PT obesity, diabetes mellitus, thalassemia, Crohn's disease.
XX
PS Claim 12; SEQ ID NO 57; 200pp; English.
XX
CC The invention describes an isolated secreted and transmembrane PRO
CC polypeptide (I) having at least 80% amino acid sequence identity to fully
CC defined sequences of 246, 440, 197, 97, 273, 571, 209, 888, 502, 310,
CC 251, 800, 507, 248, 223, 134, 136, 468, 322, 221, 194, 125 or 339 amino
CC acids as given in the specification. (I) is useful for tissue typing, as
CC molecular weight markers or as therapeutic agents. A polynucleotide (II)
CC encoding (I) is useful for chromosome identification, gene therapy,
CC tissue typing or as hybridisation probes in chromosome and gene mapping.
CC PRO1484, PRO1890, PRO1887, PRO4353, PRO4357, PRO4405, PRO5737 and PRO5990
CC is useful for treating sports injuries and arthritis. PRO1484, PRO1122,
CC PRO1889, PRO4357, PRO4380 and PRO4356 are useful for treating diabetes.
CC PRO4334, PRO4425, PRO4424, PRO4430, PRO1890, PRO1785 and PRO4422 are
CC useful for treating obesity, diabetes or hyper- or hypo-insulinaemia.
CC PRO4352, PRO4354, PRO4408, PRO6030 and PRO4499 are useful for treating
CC thalassaemia. PRO4380, PRO4408 and PRO4425 are useful for treating Berger
CC disease, Schonlein-Henoch purpura, celiac disease, dermatitis
CC herpetiformis or Crohn's disease. This is the amino acid sequence of a
CC novel human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 507 AA;

Query Match 96.9%; Score 492; DB 7; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
               ||||||||||||
Db        496 FAAFFLEMAQLH 507
```

RESULT 20
ADF09256
ID ADF09256 standard; protein; 507 AA.
XX
AC ADF09256;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human secreted and transmembrane protein PRO4380.
XX
KW cytostatic; gene therapy; human; secreted and transmembrane; PRO; cancer;

KW tumour; chromosome mapping; gene mapping; therapeutic reagent.
XX
OS Homo sapiens.
XX
PN US2003134327-A1.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2001; 2001US-00035977.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 15-DEC-1998; 98US-0112514P.
PR 22-DEC-1998; 98US-0113300P.
PR 23-DEC-1998; 98US-0113430P.
PR 23-DEC-1998; 98US-0113605P.
PR 23-DEC-1998; 98US-0113621P.
PR 23-DEC-1998; 98US-0114140P.
PR 12-JAN-1999; 99US-0115552P.
PR 22-JAN-1999; 99US-0116843P.
PR 23-MAR-1999; 99US-0125774P.
PR 23-MAR-1999; 99US-0125778P.
PR 24-MAR-1999; 99US-0125826P.
PR 31-MAR-1999; 99US-0127035P.
PR 05-APR-1999; 99US-0127706P.
PR 13-APR-1999; 99US-0129122P.
PR 21-APR-1999; 99US-0130359P.
PR 27-APR-1999; 99US-0131270P.
PR 27-APR-1999; 99US-0131272P.
PR 27-APR-1999; 99US-0131291P.
PR 04-MAY-1999; 99US-0132371P.
PR 04-MAY-1999; 99US-0132379P.
PR 04-MAY-1999; 99US-0132383P.
PR 14-MAY-1999; 99WO-US010733.
PR 25-MAY-1999; 99US-0135750P.
PR 08-JUN-1999; 99US-0138166P.
PR 20-JUL-1999; 99US-0144791P.
PR 03-AUG-1999; 99US-0146970P.
PR 29-OCT-1999; 99US-0162506P.
PR 02-DEC-1999; 99WO-US028551.
PR 22-DEC-1999; 99WO-US030720.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 16-AUG-2001; 2001US-00931836.
XX
PA (GETH) GENENTECH INC.
XX
PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2004-031325/03.
DR N-PSDB; ADF09255.
XX
PT Twenty three nucleic acids encoding PRO polypeptides, useful in
PT chromosome and gene mapping, in generating antisense RNA and DNA and in
PT gene therapy.
XX
PS Claim 12; SEQ ID NO 57; 261pp; English.
XX
CC The invention describes 23 nucleic acids encoding human secreted and
CC transmembrane PRO polypeptides. The PRO polypeptides and nucleic acids
CC are useful for the therapeutic treatment of cancerous tumours. The PRO
CC polynucleotide is useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA, and in gene therapy. The polynucleotide may also
CC be used in preparing PRO polypeptides by recombinant techniques, and in
CC generating either transgenic animals or knock-out animals which, in turn,
CC are useful in the development and screening of therapeutically useful
CC reagents. This is the amino acid sequence of a novel human secreted and
CC transmembrane protein PRO1484.
XX
SQ Sequence 507 AA;

Query Match 96.9%; Score 492; DB 8; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
               ||||||||||||
Db        496 FAAFFLEMAQLH 507
```

RESULT 21
ADW12488
ID ADW12488 standard; protein; 507 AA.
XX
AC ADW12488;
XX
DT 24-MAR-2005 (first entry)
XX
DE Human PRO4380 protein.
XX
KW PRO protein; cancer; gene therapy; cytostatic; neoplasm; cell signaling;
KW biosensor; bioreactor; photoreactor; pharmaceutical; diagnostic; PRO4380.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .26
FT /label= Signal_peptide
FT Protein 27. .507
FT /note= "Human mature PRO4380 protein"
FT Modified-site 89. .95
FT /note= "N-myristoylation site"

```
FT   Modified-site   119. .125
FT                   /note= "N-myristoylation site"
FT   Region          140. .143
FT                   /note= "Cell attachment sequence"
FT   Region          156. .167
FT                   /note= "ArgE / dapE /ACY1 / CPG "
FT   Modified-site   162. .168
FT                   /note= "N-myristoylation site"
FT   Modified-site   197. .203
FT                   /note= "N-myristoylation site"
FT   Modified-site   242. .248
FT                   /note= "N-myristoylation site"
FT   Modified-site   263. .269
FT                   /note= "N-myristoylation site"
FT   Domain          273. .292
FT                   /note = Transmembrane domain
FT   Modified-site   322. .326
FT                   /note= "N-glycosylation site"
FT   Modified-site   351. .357
FT                   /note= "N-myristoylation site"
FT   Modified-site   382. .386
FT                   /note= "N-glycosylation site"
FT   Modified-site   400. .404
FT                   /note= "cAMP and cGMP-dependent protein kinase
FT                   phosphorylation site"
FT   Modified-site   402. .406
FT                   /note= "N-glycosylation site"
XX
PN   US2004265966-A1.
XX
PD   30-DEC-2004.
XX
PF   01-JUL-2004; 2004US-00884091.
XX
PR   01-MAR-2000; 2000WO-US005601.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   09-JUL-2001; 2001WO-US021735.
PR   18-JUL-2001; 2001US-00908827.
PR   16-AUG-2001; 2001US-00931836.
XX
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (PANJ/) PAN J.
PA   (STEW/) STEWART T A.
PA   (WATA/) WATANABE C K.
PA   (WOOD/) WOOD W I.
PA   (ZHAN/) ZHANG Z.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2005-064903/07.
DR   N-PSDB; ADW12487.
XX
PT   New PRO nucleic acid or polypeptide, useful for preparing a medicament
PT   for treating a condition associated with PRO nucleic acid or polypeptide
PT   e.g., cancer.
XX
PS   Claim 12; SEQ ID NO 57; 183pp; English.
XX
CC   The present invention relates to a PRO proteins and their encoding
CC   nucleic acids. The invention is useful for preparing a medicament for
CC   treating a condition associated with PRO nucleic acid e.g., cancer. The
CC   invention is also useful in gene therapy. The present sequence is human
CC   PRO protein.
XX
SQ   Sequence 507 AA;

  Query Match             96.9%;  Score 492;  DB 9;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 22
AEB45360
ID   AEB45360 standard; protein; 507 AA.
XX
AC   AEB45360;
XX
DT   22-SEP-2005  (first entry)
XX
DE   Human wild-type carnosinase 1 protein.
XX
KW   carnosine metabolism; diabetic nephropathy; neurological disease;
KW   carnosinase 1; CN1; screening; kidney; antidiabetic; neuroprotective;
KW   nephrotropic; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2005064013-A1.
XX
PD   14-JUL-2005.
XX
PF   23-DEC-2004; 2004WO-EP014696.
XX
PR   23-DEC-2003; 2003DE-01060956.
PR   12-NOV-2004; 2004EP-00027020.
XX
PA   (JANS/) JANSSEN B.
PA   (VWOU/) VAN DER WOUDE F.
XX
PI   Janssen B,  Van Der Woude F,  Yard B,  Peters V,  Hohenadel D;
PI   Koeppel H,  Baelde H,  De Heer E,  Bakker S,  Brinkkoetter P;
XX
DR   WPI; 2005-522580/53.
DR   N-PSDB; AEB45359.
```

```
XX
PT   Use of carnosine metabolism-associated genes, for determining genetic
PT   predisposition/susceptibility to diabetic nephropathy.
XX
PS   Disclosure; Fig 1; 48pp; English.
XX
CC   The invention relates to the use of one or more genes associated with
CC   carnosine metabolism, and/or their variants, and/or their parts, and/or
CC   their 5' and/or 3' flanking regions, for determining diabetic nephropathy
CC   (DN), or an early stage of DN, or a predisposition/susceptibility to DN.
CC   Also described are: (1) a method of determining diabetic nephropathy, or
CC   an early stage of DN, or a predisposition/susceptibility to the
CC   development of DN, or a predisposition/susceptibility to DN; (2) a kit
CC   for determining DN, or an early stage of DN, or a
CC   predisposition/susceptibility to DN, containing one or more reagents for
CC   the determination of the configuration/condition/status of a nucleic acid
CC   associated with carnosine metabolism, at the genomic, transcriptional,
CC   translation and/or post-translational level in a patient sample; and (3)
CC   a method for identifying compounds for the treatment and/or prevention of
CC   DN. The gene associated with carnosine metabolism is the carnosinase 1
CC   (CN1) gene and/or the carnosinase 2 (CN2) gene. The method and kit of the
CC   invention are useful for determining diabetic nephropathy (DN), or an
CC   early stage of DN, or a predisposition/susceptibility to DN. The
CC   screening method is useful for identifying compounds for treating and/or
CC   preventing DN. The method of the invention provides a reliable way of
CC   diagnosing diabetic nephropathy without the need for kidney biopsy. The
CC   disease can be detected at an early stage allowing preventive and/or
CC   therapeutic measures to be started earlier. This sequence represents
CC   human wild-type CN1 protein.
XX
SQ   Sequence 507 AA;

  Query Match             96.9%;  Score 492;  DB 9;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507
```

```
RESULT 23
AAU28396
ID   AAU28396 standard; protein; 501 AA.
XX
AC   AAU28396;
XX
DT   03-JAN-2002  (first entry)
XX
DE   Amino acid sequence for DPI-45 and DPI-213.
XX
KW   Human; depression associated protein isoform; tryptic digest peptide;
KW   DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
KW   neuropsychiatric disorder; bipolar mood disorder; neuroleptic; DPI-213;
KW   maniac-depressive illness; schizoaffective disorder; DPI-45.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /label= Signal_peptide
FT   Protein         21. .501
FT                   /label= Mature_DPI-45_and_DPI-213
FT   Peptide         49. .63
FT                   /label= Tryptic_peptide
FT                   /note= "Specifically claimed in claim 4"
FT   Misc-difference 70
FT                   /label= Unknown
FT                   /note= "Encoded by ANA"
FT   Peptide         306. .315
FT                   /label= Tryptic_peptide
FT                   /note= "Specifically claimed in claim 4"
XX
PN   WO200162787-A1.
XX
PD   30-AUG-2001.
XX
PF   23-FEB-2001; 2001WO-GB000786.
XX
PR   24-FEB-2000; 2000GB-00004412.
PR   08-DEC-2000; 2000GB-00030050.
PR   12-DEC-2000; 2000US-0254830P.
XX
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI   Herath HMAC,  Parekh RB,  Rohlff C,  Terrett JA,  Tyson KL;
XX
DR   WPI; 2001-570626/64.
DR   N-PSDB; AAS12574.
XX
PT   Novel nucleic acid encoding a protein associated with bipolar affective
PT   disorder, which is used for diagnosis, prophylaxis and therapy of
PT   neuropsychiatric disorders, such as bipolar affective disorder.
XX
PS   Disclosure; Fig 2B; 153pp; English.
XX
CC   The present invention relates to the identification of depression
CC   associated protein isoforms (DPIs), particularly the tryptic digest
CC   peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
CC   described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
CC   affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
CC   increased in BAD subjects. Also described are peptide sequences
CC   identified from DPI-45 and DPI-213 and the nucleic acid sequence they are
CC   encoded by. The sequences of the invention are useful for clinical
CC   screening, diagnosis, prognosis, therapy and prophylaxis of
CC   neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
CC   BP), maniac-depressive illnesses, attention deficit disorders,
CC   schizoaffective disorders, and unipolar affective disorders. The present
CC   sequence represents the amino acid sequence for DPI-45 and DPI-213
XX
SQ   Sequence 501 AA;

  Query Match             84.4%;  Score 429;  DB 4;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0;
```

```
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 130

Qy        138 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 190

Qy        198 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250

Qy        258 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310

Qy        318 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370

Qy        378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 430

Qy        438 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490

Qy        498 AAFFLEMAQ 506
              |||||||||
Db        491 AAFFLEMAQ 499


RESULT 24
AAU25426
ID   AAU25426 standard; protein; 501 AA.
XX
AC   AAU25426;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human Schizophrenia-Associated Protein Isoform (SPI) 238/240.
XX
KW   Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
KW   neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
XX
OS   Homo sapiens.
XX
PN   WO200162785-A2.
XX
PD   30-AUG-2001.
XX
PF   23-FEB-2001; 2001WO-GB000792.
XX
PR   24-FEB-2000; 2000GB-00004415.
PR   28-DEC-2000; 2000US-00750395.
XX
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI   Herath HMAC,  Parekh RB,  Rohlff C,  Terrett JA,  Tyson KL;
XX
DR   WPI; 2001-570624/64.
DR   N-PSDB; AAS42478.
XX
PT   New schizophrenia associated protein isoforms and encoding nucleic acid
PT   molecules, useful for treatment, diagnosis and prognosis of schizophrenia
PT   and screening for potential drugs for treatment and new drug targets.
XX
PS   Disclosure; Fig 4A; 148pp; English.
XX
CC   The sequence represents a schizophrenia-associated protein isoform (SPI).
CC   These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
CC   in cerebrospinal fluid, serum or plasma and are useful markers of
CC   schizophrenia. The sequences can be used for treatment and diagnosis of
CC   schizophrenia, screening, prognosis, monitoring the results of therapy,
CC   identifying patients most likely to respond to a particular therapy and
CC   identification of new targets for drug treatment. SPI DNA is useful as a
CC   nucleic acid probe to detect the presence of nucleic acids or SPIs
XX
SQ   Sequence 501 AA;

  Query Match             84.4%;  Score 429;  DB 4;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 130

Qy        138 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 190

Qy        198 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250

Qy        258 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310

Qy        318 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370

Qy        378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 430

Qy        438 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490

Qy        498 AAFFLEMAQ 506
              |||||||||
Db        491 AAFFLEMAQ 499


RESULT 25
AAU15115
ID   AAU15115 standard; protein; 501 AA.
XX
AC   AAU15115;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Schizophrenia-associated isoform SPI-238/240.
XX
KW   Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KW   neurological disorder; neuropathy.
XX
OS   Homo sapiens.
XX
PN   WO200163293-A2.
XX
PD   30-AUG-2001.
XX
PF   23-FEB-2001; 2001WO-GB000783.
XX
PR   24-FEB-2000; 2000GB-00004415.
PR   28-DEC-2000; 2000US-00750395.
XX
PA   (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
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PI   Herath HMAC,  Parekh RB,  Rohlff C;
XX
DR   WPI; 2001-502868/55.
DR   N-PSDB; AAS23811.
XX
PT   Diagnosing and monitoring Schizophrenia by detecting the presence of
PT   Schizophrenia Associated Features and Schizophrenia Associated Protein
PT   Isoforms in samples of cerebrospinal fluid.
XX
PS   Claim 8; Fig 4A; 160pp; English.
XX
CC   The invention relates to methods and compositions for screening,
CC   diagnosis and prognosis of Schizophrenia. The method involves detecting
CC   the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH
CC   Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
CC   immunoassay or hybridisation assay, for diagnosing and monitoring SCH,
CC   studying the effectiveness of treatments and for identifying potential
CC   therapeutic agents. The method is used for (1) screening or diagnosis of
CC   SCH and the relative abundance of at least 1 chosen feature correlates
CC   with the presence or absence of SCH; and (2) monitoring the effect of
CC   therapy administered to a subject with SCH and the relative abundance of
CC   at least 1 chosen feature which correlates with the severity of SCH. The
CC   expression and activity of the SFs, SPIs and related molecules (e.g.
CC   secondary messengers) are studied to diagnose SCH, monitor the progress
CC   of the disorder and the effectiveness of treatment and as targets to
CC   identify and produce potential therapeutic agents for the treatment of
CC   SCH. The paucity of detectable neuralgic defects distinguishes
CC   neuropsychiatric disorders such as SCH from neurological disorders, where
CC   manifestations of anatomical and biochemical changes have been identified
CC   in many cases. Consequently the identification and characterisation of
CC   cellular and/or molecular causative defects and neuropathies are
CC   necessary for improved treatment of neuropsychiatric disorders. AAU15114-
CC   AAU15762 represent the amino acid sequences of schizophrenia-associated
CC   isoforms used in the method of the invention
XX
SQ   Sequence 501 AA;

  Query Match             84.4%;  Score 429;  DB 4;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 130

Qy        138 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 190

Qy        198 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250

Qy        258 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310

Qy        318 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370

Qy        378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 430

Qy        438 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490

Qy        498 AAFFLEMAQ 506
              |||||||||
Db        491 AAFFLEMAQ 499
```

```
RESULT 26
ADO79056
ID   ADO79056 standard; protein; 501 AA.
XX
AC   ADO79056;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Schizophrenia-Associated Protein Isoform SPI-238/SPI-240.
XX
KW   neuroleptic; Schizophrenia; immunospecific binding;
KW   Schizophrenia-Associated Protein Isoform; SPI; schizophrenia screening;
KW   schizophrenia diagnosing; schizophrenia prognosing;
KW   Schizophrenia treatment; drug development; cerebrospinal fluid; human;
KW   SPI-238; SPI-240.
XX
OS   Homo sapiens.
XX
PN   US2004110938-A1.
XX
PD   10-JUN-2004.
XX
PF   23-FEB-2001; 2001US-00791377.
XX
PR   24-FEB-2000; 2000GB-00044156.
PR   28-DEC-2000; 2000US-00750395.
XX
PA   (PARE/) PAREKH R B.
PA   (HERA/) CHANDRASIRI HERATH H M A.
PA   (ROHL/) ROHLFF C.
PA   (TERR/) TERRETT J A.
PA   (TYSO/) TYSON K L.
XX
PI   Parekh RB,  Chandrasiri Herath HMA,  Rohlff C,  Terrett JA,  Tyson KL;
XX
DR   WPI; 2004-440403/41.
DR   N-PSDB; ADO79056.
XX
PT   New isolated nucleic acid molecule, useful for diagnosing Schizophrenia,
PT   for monitoring the effectiveness of Schizophrenia treatment or for
PT   screening agents for treating Schizophrenia.
XX
PS   Disclosure; SEQ ID NO 674; 170pp; English.
XX
CC   The invention describes an isolated nucleic acid molecule (I) that
CC   hybridises to two short nucleic acid sequences and the 1515 amino acid
CC   sequence fully defined in the specification. Also described are: a
CC   preparation comprising an isolated peptide coded for by the nucleic acid
CC   molecule above, or comprising an isolated human protein comprising one or
CC   more of the following sequences: Glu-Leu-Asp-Val-Leu-Gln-Gly-Arg, and Gly
CC   -Ile-Leu-Ile-Leu-Gly-Gln-Glu-Gln-Asp-Thr-Leu-Gly-Gly-Arg; methods for
CC   diagnosing Schizophrenia; antibodies capable of immunospecific binding to
CC   a Schizophrenia-Associated Protein Isoform (SPI); methods of treating
CC   Schizophrenia; and methods of screening for agents that modulate a
CC   characteristic (e.g., expression or binding activity) of an SPI, an SPI
CC   analogue, or an SPI-related polypeptide. The nucleic acid molecule and
CC   encoded proteins, as well as the methods and compositions are useful for
CC   screening, diagnosing, and prognosing Schizophrenia, for monitoring the
CC   effectiveness of Schizophrenia treatment, for identifying patients most
CC   likely to respond to a particular therapeutic treatment and for
CC   developing drug. They are also useful for screening modulators of
CC   Schizophrenia-Associated Protein Isoform useful for treating
CC   Schizophrenia. This is the amino acid sequence of schizophrenia-
CC   associated protein isoform SPI-238/SPI-240 fusion.
XX
SQ   Sequence 501 AA;

  Query Match             84.4%;  Score 429;  DB 8;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 137
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 130

Qy        138 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 197
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 190

Qy        198 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 257
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250

Qy        258 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 317
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310

Qy        318 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370

Qy        378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 437
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 430

Qy        438 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 497
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490

Qy        498 AAFFLEMAQ 506
                |||||||||
Db        491 AAFFLEMAQ 499
```

```
RESULT 27
AAB18921
ID   AAB18921 standard; protein; 507 AA.
XX
AC   AAB18921;
XX
DT   08-FEB-2001  (first entry)
XX
DE   A novel polypeptide designated PRO4380.
XX
KW   Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW   PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW   PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;
KW   PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW   insulinemia; kidney disorder; Bergers disease; nephropathy;
KW   Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW   Crohns disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .26
FT                   /note= "signal sequence"
FT   Modified-site   89. .95
FT                   /note= "N-myristoylation site"
FT   Modified-site   119. .125
FT                   /note= "N-myristoylation site"
FT   Modified-site   162. .168
FT                   /note= "N-myristoylation site"
FT   Modified-site   197. .203
FT                   /note= "N-myristoylation site"
FT   Misc-difference 230
FT                   /note= "Ile encoded by CTG"
FT   Modified-site   242. .248
FT                   /note= "N-myristoylation site"
FT   Modified-site   263. .269
FT                   /note= "N-myristoylation site"
FT   Domain          273. .292
FT                   /note= "transmembrane domain"
FT   Modified-site   322. .326
FT                   /note= "N-glycosylation site"
FT   Modified-site   351. .357
FT                   /note= "N-myristoylation site"
FT   Modified-site   382. .386
FT                   /note= "N-glycosylation site"
FT   Modified-site   400. .404
FT                   /note= "cAMP- and cGMP-dependent protein kinase"
FT   Modified-site   402. .406
FT                   /note= "N-glycosylation site"
XX
PN   WO200056889-A2.
XX
PD   28-SEP-2000.
XX
PF   01-MAR-2000; 2000WO-US005601.
XX
PR   23-MAR-1999;   99US-0125774P.
PR   23-MAR-1999;   99US-0125778P.
PR   24-MAR-1999;   99US-0125826P.
PR   31-MAR-1999;   99US-0127035P.
PR   05-APR-1999;   99US-0127706P.
PR   21-APR-1999;   99US-0130359P.
PR   27-APR-1999;   99US-0131270P.
PR   27-APR-1999;   99US-0131272P.
PR   27-APR-1999;   99US-0131291P.
PR   04-MAY-1999;   99US-0132371P.
PR   04-MAY-1999;   99US-0132379P.
PR   04-MAY-1999;   99US-0132383P.
PR   25-MAY-1999;   99US-0135750P.
PR   08-JUN-1999;   99US-0138166P.
PR   20-JUL-1999;   99US-0144791P.
PR   03-AUG-1999;   99US-0146970P.
PR   09-DEC-1999;   99US-0170262P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Desnoyers L,  Eaton DL,  Goddard A,  Godowski PJ,  Gurney AL,  Pan J;
PI   Stewart TA,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2000-628263/60.
DR   N-PSDB; AAA96348.
XX
PT   Novel secreted and transmembrane polypeptides useful for diagnosing tumor
PT   in a mammal, for identifying agonists and antagonists of the polypeptide
PT   and for therapeutic use.
XX
PS   Claim 12; Fig 26; 222pp; English.
XX
CC   The present sequence represents a secreted or transmembrane polypeptide.
CC   The specification describes polypeptides designated PRO1484, PRO4334,
CC   PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC   PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC   PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC   useful for diagnosing tumour in a mammal. The polypeptides, their
CC   agonists and antagonists are useful treating a condition associated with
CC   expression or activity of the polypeptide. Conditions treated include
CC   obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are
CC   capable of inducing proliferation of mammalian kidney mesangial cells and
CC   are therefore useful for treating kidney disorders associated with
CC   decreased mesangial cell function such as Bergers disease or other
CC   nephropathies associated with Schonlein-Henoch purpura, celiac disease,
CC   dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC   to generate transgenic animals for use in development and screening of
CC   therapeutically useful reagents and also for chromosome identification
CC   and tissue typing
XX
SQ   Sequence 507 AA;

  Query Match             77.0%;  Score 391;  DB 3;  Length 507;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  491;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNIWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507
```

RESULT 28
AAM40149
ID AAM40149 standard; protein; 342 AA.
XX
AC AAM40149;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 3294.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59305.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 5; SEQ ID NO 3294; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 342 AA;

Query Match 66.1%; Score 336; DB 4; Length 342;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        173 AWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLW 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 AWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLW 66

Qy        233 ISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHIL 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 ISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHIL 126

Qy        293 VPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHG 352
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 VPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHG 186

Qy        353 IEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSM 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 IEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSM 246

Qy        413 TLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLG 472
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 TLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLG 306

Qy        473 AVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||||||||||
Db        307 AVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQLH 342
```

RESULT 29
AAM41935
ID AAM41935 standard; protein; 358 AA.
XX
AC AAM41935;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 6866.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

```
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US034263.
XX
PR   23-DEC-1999;   99US-00471275.
PR   21-JAN-2000; 2000US-00488725.
PR   25-APR-2000; 2000US-00552317.
PR   20-JUN-2000; 2000US-00598042.
PR   19-JUL-2000; 2000US-00620312.
PR   03-AUG-2000; 2000US-00653450.
PR   14-SEP-2000; 2000US-00662191.
PR   19-OCT-2000; 2000US-00693036.
PR   29-NOV-2000; 2000US-00727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J,  Zhao QA;
PI   Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI61091.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders such
PT   as central nervous system injuries.
XX
PS   Example 2; SEQ ID NO 6866; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC   encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders. Note: The sequence data for this patent did not form
CC   part of the printed specification
XX
SQ   Sequence 358 AA;

  Query Match             64.2%;  Score 326;  DB 4;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-316;
  Matches  326;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        303 LTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGT 362
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Qy        363 KTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIAN 422
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Qy        483 EKINRWNYIEGTKLFAAFFLEMAQLH 508
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Db        333 EKINRWNYIEGTKLFAAFFLEMAQLH 358


RESULT 30
ADC77691
ID   ADC77691 standard; protein; 508 AA.
XX
AC   ADC77691;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Human 55054 protein SEQ ID NO:54.
XX
KW   pain disorder; pain signalling mechanism; analgesic; antimigraine;
KW   antiinflammatory; gene therapy; inflammatory pain; chronic pain;
KW   neuropathic pain; neuralgia; fibromyalgia; cancer pain; migraine;
KW   headache; pain; human.
XX
OS   Homo sapiens.
XX
PN   WO2003073983-A2.
XX
PD   12-SEP-2003.
XX
PF   19-FEB-2003; 2003WO-US004816.
XX
PR   28-FEB-2002; 2002US-0360495P.
PR   04-APR-2002; 2002US-0370121P.
PR   16-APR-2002; 2002US-0373010P.
PR   19-APR-2002; 2002US-0373908P.
PR   03-MAY-2002; 2002US-0377717P.
PR   13-MAY-2002; 2002US-0379949P.
PR   21-MAY-2002; 2002US-0382409P.
PR   03-JUN-2002; 2002US-0385280P.
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PR   10-JUN-2002; 2002US-0387536P.
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PR   21-AUG-2002; 2002US-0404996P.
PR   19-SEP-2002; 2002US-0412006P.
PR   09-OCT-2002; 2002US-0417327P.
PR   10-OCT-2002; 2002US-0417499P.
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PR   10-DEC-2002; 2002US-0432320P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Rosenfeld JB,  Silos-Santiago I;
XX
DR   WPI; 2003-712843/67.
DR   N-PSDB; ADC77690.
XX
PT   Identifying a compound capable of treating a pain disorder e.g.,
PT   neuropathic pain comprises assaying the ability of the compound to
PT   modulate the nucleic acid expression or polypeptide activity.
XX
PS   Claim 1; SEQ ID NO 54; 277pp; English.
XX
CC   The present invention describes a method for identifying a compound (C)
CC   capable of treating a pain disorder comprising assaying the ability of
CC   the compound to modulate 9949, 14230, 760, 62553, 12216, 17719, 41897,
CC   47174, 33408, 10002, 16209, 314, 636, 27410, 33260, 619, or 13424 nucleic
CC   acid expression or 9949, 14230, 760, 62553, 12216, 17719, 41897, 47174,
CC   33408, 10002, 16209, 314, 636, 27410, 33260, 619, 15985, polypeptide
CC   activity. Also described: (1) identifying a compound (C) capable of
CC   modulating a pain signalling mechanism; and (2) treating a subject having
CC   a pain disorder characterised by aberrant nucleic acid expression or
CC   polypeptide activity. (C) has analgesic, antimigraine and
CC   antiinflammatory activities, and can be used in gene therapy. The method
```

CC is useful for identifying a modulator compound capable of treating a pain
CC disorder, e.g. inflammatory pain, chronic pain, neuropathic pain,
CC neuralgia, fibromyalgia, cancer pain, migraine/headache pain or tissue
CC pain comprising administering the modulator to a subject having a pain
CC disorder characterised by aberrant nucleic acid expression or polypeptide
CC activity. The present sequence represents the human 55054 protein from
CC the present invention.
XX
SQ Sequence 508 AA;

Query Match 46.3%; Score 235; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.3e-225;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        334 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 393
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Qy        394 HLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 453
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Qy        454 IAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQLH 508
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Db        454 IAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQLH 508
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Search completed: March 30, 2006, 09:07:53
Job time : 197 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 30, 2006, 09:12:07 ; Search time 46 Seconds
(without alignments)
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Title: US-10-849-979-139
Perfect score: 508
Sequence: 1 MDPKLGRMAASLLAVLLLLL.....NYIEGTKLFAAFFLEMAQLH 508

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 6

Total number of hits satisfying chosen parameters: 4086

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	119	23.4	148	2	US-09-621-976-3957	Sequence 3957, Ap
2	11	2.2	429	2	US-09-270-767-45937	Sequence 45937, A
3	10	2.0	318	2	US-09-581-005-2	Sequence 2, Appli
4	9	1.8	258	2	US-09-134-000C-4891	Sequence 4891, Ap
5	9	1.8	841	2	US-09-538-092-67	Sequence 67, Appl
6	8	1.6	16	2	US-09-434-345-4	Sequence 4, Appli
7	8	1.6	78	2	US-10-178-213-278	Sequence 278, App
8	8	1.6	82	2	US-10-178-213-56	Sequence 56, Appl
9	8	1.6	100	2	US-09-950-933A-40	Sequence 40, Appl
10	8	1.6	107	2	US-09-270-767-40343	Sequence 40343, A
11	8	1.6	107	2	US-09-270-767-55559	Sequence 55559, A
12	8	1.6	115	2	US-09-461-325-160	Sequence 160, App
13	8	1.6	115	2	US-10-012-542-160	Sequence 160, App
14	8	1.6	115	2	US-10-115-123-160	Sequence 160, App
15	8	1.6	115	2	US-09-991-181-95	Sequence 95, Appl
16	8	1.6	115	2	US-09-990-444-95	Sequence 95, Appl
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18	8	1.6	115	2	US-09-992-598-95	Sequence 95, Appl
19	8	1.6	125	2	US-09-621-976-3958	Sequence 3958, Ap
20	8	1.6	136	2	US-09-893-737-150	Sequence 150, App
21	8	1.6	190	2	US-09-893-737-198	Sequence 198, App
22	8	1.6	254	2	US-09-543-681A-7981	Sequence 7981, Ap
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24	8	1.6	277	2	US-09-431-887-34	Sequence 34, Appl
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133	7	1.4	174	2	US-09-823-038A-12	Sequence 12, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 3957, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 3957
;   LENGTH: 148
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -27..-1
;   NAME/KEY: UNSURE
;   LOCATION: 93
;   OTHER INFORMATION: Xaa =  * ,Cys,Asp,Glu,Phe,Gly,Leu,Val,Trp,Tyr
;   NAME/KEY: UNSURE
;   LOCATION: 99
;   OTHER INFORMATION: Xaa = Ala,Cys,Asp,Phe,Gly,His,Ile,Leu,Asn,Pro,Arg,Ser,Thr,Val,Tyr
;   NAME/KEY: UNSURE
;   LOCATION: 102
;   OTHER INFORMATION: Xaa = Cys,Ser
;   NAME/KEY: UNSURE
;   LOCATION: 98
;   OTHER INFORMATION: Xaa = Lys,Asn,Arg,Ser,Thr
US-09-621-976-3957

  Query Match             23.4%;  Score 119;  DB 2;  Length 148;
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RESULT 2
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; Sequence 45937, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45937
;   LENGTH: 429
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-45937

  Query Match              2.2%;  Score 11;  DB 2;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 0.056;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 VIGKFSIRLVP 380
              ||||||||||| 
Db        292 VIGKFSIRLVP 302


RESULT 3
US-09-581-005-2
; Sequence 2, Application US/09581005
; Patent No. 6825028
; GENERAL INFORMATION:
;  APPLICANT: von Eichel-Streiber, Christoph
;  APPLICANT:  Chakraborty, Trinad
;  TITLE OF INVENTION: TGC Method For Inducting Targeted Somatic Transgenesis
;  FILE REFERENCE: E 52 P2 Wo
;  CURRENT APPLICATION NUMBER: US/09/581,005
;  CURRENT FILING DATE:  2000-06-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 318
;   TYPE: PRT
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; ORGANISM: Listeria monocytogenes Strain EGD1/2a
US-09-581-005-2

Query Match 2.0%; Score 10; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 GKLYGRGATD 166
||||||||||
Db 33 GKLYGRGATD 42

RESULT 4
US-09-134-000C-4891
; Sequence 4891, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4891
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4891

Query Match 1.8%; Score 9; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 KLYGRGATD 166
|||||||||
Db 128 KLYGRGATD 136

RESULT 5
US-09-538-092-67
; Sequence 67, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 67
; LENGTH: 841
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YCL054W
US-09-538-092-67

Query Match 1.8%; Score 9; DB 2; Length 841;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 299 EVVPLTEEE 307
|||||||||
Db 342 EVVPLTEEE 350

RESULT 6
US-09-434-345-4
; Sequence 4, Application US/09434345
; Patent No. 6511676
; GENERAL INFORMATION:
; APPLICANT: Boulikas, Teni
; TITLE OF INVENTION: THERAPY FOR HUMAN CANCERS USING
; TITLE OF INVENTION: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO
; TITLE OF INVENTION: LIPOSOMES
; FILE REFERENCE: TB 2001.00
; CURRENT APPLICATION NUMBER: US/09/434,345
; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Duck Hepatitis B Virus
US-09-434-345-4

Query Match 1.6%; Score 8; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 SGTFGGIL 270
||||||||
Db 2 SGTFGGIL 9

RESULT 7
US-10-178-213-278
; Sequence 278, Application US/10178213
; Patent No. 6911577
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/10/178,213
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-178-213-278

Query Match 1.6%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLL 21
|||||||
Db 10 AVLLLLL 17

```
RESULT 8
US-10-178-213-56
; Sequence 56, Application US/10178213
; Patent No. 6911577
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
;   LENGTH: 82
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-10-178-213-56

  Query Match             1.6%;  Score 8;  DB 2;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 9.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AVLLLLLL 21
              ||||||||
Db         12 AVLLLLLL 19


RESULT 9
US-09-950-933A-40
; Sequence 40, Application US/09950933A
; Patent No. 6875907
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro, Pedro
;  TITLE OF INVENTION: Antimicrobial Peptides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/238472
;  CURRENT APPLICATION NUMBER: US/09/950,933A
;  CURRENT FILING DATE:  2001-09-11
;  PRIOR APPLICATION NUMBER: 60/232,569
;  PRIOR FILING DATE: 2000-09-13
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
;   LENGTH: 100
;   TYPE: PRT
;   ORGANISM: Zea mays
US-09-950-933A-40

  Query Match             1.6%;  Score 8;  DB 2;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AVLLLLLL 21
              ||||||||
Db         12 AVLLLLLL 19


RESULT 10
US-09-270-767-40343
; Sequence 40343, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40343
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-40343

  Query Match             1.6%;  Score 8;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 LAVLLLLL 20
              ||||||||
Db         80 LAVLLLLL 87


RESULT 11
US-09-270-767-55559
; Sequence 55559, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55559
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-55559

  Query Match             1.6%;  Score 8;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 LAVLLLLL 20
              ||||||||
Db         80 LAVLLLLL 87


RESULT 12
US-09-461-325-160
; Sequence 160, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/09/461,325A
;  CURRENT FILING DATE: 1999-12-14
;  EARLIER APPLICATION NUMBER: PCT/US99/13418
;  EARLIER FILING DATE: 1999-06-15
;  EARLIER APPLICATION NUMBER: 60/089,507
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,508
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,509
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/089,510
;  EARLIER FILING DATE: 1998-06-16
;  EARLIER APPLICATION NUMBER: 60/090,112
;  EARLIER FILING DATE: 1998-06-22
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;  EARLIER APPLICATION NUMBER: 60/090,113
;  EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (96)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (100)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-160

  Query Match             1.6%;  Score 8;  DB 2;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AVLLLLLL 21
              ||||||||
Db         20 AVLLLLLL 27


RESULT 13
US-10-012-542-160
; Sequence 160, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029P1
;  CURRENT APPLICATION NUMBER: US/10/012,542
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (96)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (100)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-012-542-160

  Query Match             1.6%;  Score 8;  DB 2;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AVLLLLLL 21
              ||||||||
Db         20 AVLLLLLL 27


RESULT 14
US-10-115-123-160
; Sequence 160, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 94 Human Secreted Proteins
;  FILE REFERENCE: PZ029G30AP1D2
;  CURRENT APPLICATION NUMBER: US/10/115,123
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: PCT/US99/13418
;  PRIOR FILING DATE: 1999-06-15
;  PRIOR APPLICATION NUMBER: 60/089,507
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,508
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,509
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/089,510
;  PRIOR FILING DATE: 1998-06-16
;  PRIOR APPLICATION NUMBER: 60/090,112
;  PRIOR FILING DATE: 1998-06-22
;  PRIOR APPLICATION NUMBER: 60/090,113
;  PRIOR FILING DATE: 1998-06-22
;  NUMBER OF SEQ ID NOS: 532
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 160
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (96)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: SITE
;   LOCATION: (100)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-115-123-160

  Query Match             1.6%;  Score 8;  DB 2;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AVLLLLLL 21
              ||||||||
Db         20 AVLLLLLL 27


RESULT 15
US-09-991-181-95
; Sequence 95, Application US/09991181
; Patent No. 6913919
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676

; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
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; PRIOR FILING DATE: 1998-07-09

Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         14 AVLLLLL 21
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Db         20 AVLLLLL 27
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RESULT 16
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; Sequence 95, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Gerritsen,Mary E.
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; APPLICANT: Paoni,Nicholas F.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 18
US-09-992-598-95
; Sequence 95, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
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; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 1.6%; Score 8; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          14 AVLLLLLL 21
               ||||||||
Db          20 AVLLLLLL 27
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RESULT 19
US-09-621-976-3958
; Sequence 3958, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 3958
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -92..-1
US-09-621-976-3958

Query Match 1.6%; Score 8; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          12 LLAVLLLL 19
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Db          84 LLAVLLLL 91
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RESULT 20
US-09-893-737-150
; Sequence 150, Application US/09893737
; Patent No. 6822082
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-893-737-150

Query Match 1.6%; Score 8; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VLLLLLLE 22
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Db 3 VLLLLLLE 10

RESULT 21
US-09-893-737-198
; Sequence 198, Application US/09893737
; Patent No. 6822082
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 198
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-198

Query Match 1.6%; Score 8; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
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Db 20 AVLLLLLL 27

RESULT 22
US-09-543-681A-7981
; Sequence 7981, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7981
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7981

Query Match 1.6%; Score 8; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 PLTEEEIN 309
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Db 241 PLTEEEIN 248

RESULT 23
US-07-706-872-3
; Sequence 3, Application US/07706872
; Patent No. 5237056
; GENERAL INFORMATION:
; APPLICANT: Fischbach, Gerald D.
; TITLE OF INVENTION: Identification of a Protein Which
; TITLE OF INVENTION: Promotes the Synthesis of Acetylcholine Receptors and Uses
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/706,872
; FILING DATE: 19910529
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU91-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-706-872-3

Query Match 1.6%; Score 8; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAVLLLLL 20
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Db 253 LAVLLLLL 260

RESULT 24
US-09-431-887-34
; Sequence 34, Application US/09431887
; Patent No. 6534036
; GENERAL INFORMATION:
; APPLICANT: D-Gen Limited
; TITLE OF INVENTION: BIOLOGICAL MATERIALS AND METHODS USEFUL IN THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PRION DISEASE
; FILE REFERENCE: ICOT/P21952
; CURRENT APPLICATION NUMBER: US/09/431,887
; CURRENT FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: GB 9824091.4
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-431-887-34

Query Match 1.6%; Score 8; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAVLLLLL 20

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Db        263 LAVLLLLL 270


RESULT 25
US-09-107-532A-5519
; Sequence 5519, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 5519:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 379 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        HYPOTHETICAL: YES
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...379
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5519:
US-09-107-532A-5519

  Query Match             1.6%;  Score 8;  DB 2;  Length 379;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        159 LYGRGATD 166
              ||||||||
Db         97 LYGRGATD 104


RESULT 26
US-09-902-540-10173
; Sequence 10173, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10173
;   LENGTH: 382
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-10173

  Query Match             1.6%;  Score 8;  DB 2;  Length 382;
  Best Local Similarity   100.0%;  Pred. No. 38;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 LLAVLLLL 19
              ||||||||
Db         35 LLAVLLLL 42


RESULT 27
US-09-540-236-2685
; Sequence 2685, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR
;  TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.2005-001
;  CURRENT APPLICATION NUMBER: US/09/540,236
;  CURRENT FILING DATE: 2000-04-04
;  NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2685
;   LENGTH: 402
;   TYPE: PRT
;   ORGANISM: M.catarrhalis
US-09-540-236-2685

  Query Match             1.6%;  Score 8;  DB 2;  Length 402;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 GKLYGRGA 164
              ||||||||
Db        112 GKLYGRGA 119


RESULT 28
US-09-328-352-5309
; Sequence 5309, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5309
;   LENGTH: 406
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-5309

  Query Match             1.6%;  Score 8;  DB 2;  Length 406;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        156 DGKLYGRG 163
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Db        120 DGKLYGRG 127


RESULT 29
US-09-543-681A-5952
; Sequence 5952, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5952
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-5952

  Query Match             1.6%;  Score 8;  DB 2;  Length 470;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 VLLLLLLE 22
              ||||||||
Db         38 VLLLLLLE 45


RESULT 30
US-09-902-540-12189
; Sequence 12189, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12189
;   LENGTH: 470
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-12189

  Query Match             1.6%;  Score 8;  DB 2;  Length 470;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 LGRMAASL 12
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Db        395 LGRMAASL 402


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Job time : 48 secs
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OM protein - protein search, using sw model

Run on: March 30, 2006, 09:12:47 ; Search time 168 Seconds
(without alignments)
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Title: US-10-849-979-139
Perfect score: 508
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Searched: 1867569 seqs, 417829326 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	508	100.0	508	3	US-09-731-872-242	Sequence 242, App
2	508	100.0	508	3	US-09-948-783-139	Sequence 139, App
3	508	100.0	508	3	US-09-876-997-242	Sequence 242, App
4	508	100.0	508	5	US-10-643-836-242	Sequence 242, App
5	508	100.0	508	5	US-10-472-533-371	Sequence 371, App
6	508	100.0	509	3	US-09-892-877-137	Sequence 137, App
7	492	96.9	507	3	US-09-963-290-2	Sequence 2, Appli
8	492	96.9	507	3	US-09-931-836-57	Sequence 57, Appl
9	492	96.9	507	4	US-10-036-342-57	Sequence 57, Appl
10	492	96.9	507	4	US-10-036-041-57	Sequence 57, Appl
11	492	96.9	507	4	US-10-035-855-57	Sequence 57, Appl
12	492	96.9	507	4	US-10-036-214-57	Sequence 57, Appl
13	492	96.9	507	4	US-10-035-719-57	Sequence 57, Appl
14	492	96.9	507	4	US-10-036-160-57	Sequence 57, Appl
15	492	96.9	507	4	US-10-035-958-57	Sequence 57, Appl
16	492	96.9	507	4	US-10-036-150-57	Sequence 57, Appl
17	492	96.9	507	4	US-10-036-063-57	Sequence 57, Appl
18	492	96.9	507	4	US-10-035-977-57	Sequence 57, Appl
19	492	96.9	507	4	US-10-275-107-68	Sequence 68, Appl
20	492	96.9	507	5	US-10-884-091-57	Sequence 57, Appl
21	429	84.4	501	3	US-09-791-378-674	Sequence 674, App
22	429	84.4	501	3	US-09-791-393-2	Sequence 2, Appli
23	429	84.4	501	3	US-09-791-389-2	Sequence 2, Appli
24	429	84.4	501	3	US-09-791-377-674	Sequence 674, App
25	235	46.3	508	4	US-10-369-022-54	Sequence 54, Appl
26	126	24.8	133	4	US-10-296-115-1427	Sequence 1427, Ap
27	100	19.7	316	4	US-10-264-237-2057	Sequence 2057, Ap
28	54	10.6	100	5	US-10-450-763-32013	Sequence 32013, A
29	37	7.3	157	5	US-10-450-763-32012	Sequence 32012, A
30	15	3.0	15	3	US-09-791-378-199	Sequence 199, App
31	15	3.0	15	3	US-09-791-378-657	Sequence 657, App
32	15	3.0	15	3	US-09-791-393-297	Sequence 297, App
33	15	3.0	15	3	US-09-791-389-297	Sequence 297, App
34	15	3.0	15	3	US-09-791-377-199	Sequence 199, App
35	15	3.0	15	3	US-09-791-377-657	Sequence 657, App
36	14	2.8	14	3	US-09-791-378-201	Sequence 201, App
37	14	2.8	14	3	US-09-791-378-665	Sequence 665, App
38	14	2.8	14	3	US-09-791-377-201	Sequence 201, App
39	14	2.8	14	3	US-09-791-377-665	Sequence 665, App
40	11	2.2	11	3	US-09-791-378-200	Sequence 200, App
41	11	2.2	11	3	US-09-791-378-202	Sequence 202, App
42	11	2.2	11	3	US-09-791-378-206	Sequence 206, App
43	11	2.2	11	3	US-09-791-377-200	Sequence 200, App
44	11	2.2	11	3	US-09-791-377-202	Sequence 202, App
45	11	2.2	11	3	US-09-791-377-206	Sequence 206, App
46	11	2.2	415	6	US-11-097-143-25542	Sequence 25542, A
47	11	2.2	462	6	US-11-097-143-25548	Sequence 25548, A
48	10	2.0	10	3	US-09-791-378-203	Sequence 203, App
49	10	2.0	10	3	US-09-791-378-667	Sequence 667, App
50	10	2.0	10	3	US-09-791-393-308	Sequence 308, App
51	10	2.0	10	3	US-09-791-389-308	Sequence 308, App
52	10	2.0	10	3	US-09-791-377-203	Sequence 203, App
53	10	2.0	10	3	US-09-791-377-667	Sequence 667, App
54	10	2.0	308	4	US-10-425-114-64882	Sequence 64882, A
55	10	2.0	318	5	US-10-894-438-2	Sequence 2, Appli
56	10	2.0	608	4	US-10-425-115-232058	Sequence 232058,
57	9	1.8	9	3	US-09-791-378-204	Sequence 204, App
58	9	1.8	9	3	US-09-791-377-204	Sequence 204, App
59	9	1.8	90	4	US-10-437-963-108300	Sequence 108300,
60	9	1.8	100	4	US-10-437-963-178801	Sequence 178801,
61	9	1.8	150	4	US-10-243-552-646	Sequence 646, App
62	9	1.8	150	5	US-10-450-763-34153	Sequence 34153, A
63	9	1.8	194	4	US-10-227-884-32	Sequence 32, Appl
64	9	1.8	194	4	US-10-230-163-32	Sequence 32, Appl
65	9	1.8	194	4	US-10-230-338-32	Sequence 32, Appl
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73	9	1.8	194	4	US-10-219-076-32	Sequence 32, Appl
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81	9	1.8	194	4	US-10-230-260-32	Sequence 32, Appl
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84	9	1.8	194	4	US-10-216-165-32	Sequence 32, Appl
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115	9	1.8	194	4	US-10-219-467-32	Sequence 32, Appl
116	9	1.8	194	4	US-10-219-469-32	Sequence 32, Appl
117	9	1.8	194	4	US-10-219-471-32	Sequence 32, Appl
118	9	1.8	194	4	US-10-219-473-32	Sequence 32, Appl
119	9	1.8	194	4	US-10-219-476-32	Sequence 32, Appl
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121	9	1.8	194	4	US-10-227-874-32	Sequence 32, Appl
122	9	1.8	194	4	US-10-227-876-32	Sequence 32, Appl
123	9	1.8	194	4	US-10-227-878-32	Sequence 32, Appl
124	9	1.8	194	4	US-10-229-974-32	Sequence 32, Appl
125	9	1.8	194	4	US-10-230-024-32	Sequence 32, Appl
126	9	1.8	194	4	US-10-230-113-32	Sequence 32, Appl
127	9	1.8	194	4	US-10-230-183-32	Sequence 32, Appl
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129	9	1.8	194	4	US-10-230-306-32	Sequence 32, Appl
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131	9	1.8	194	4	US-10-230-427-32	Sequence 32, Appl
132	9	1.8	194	4	US-10-230-433-32	Sequence 32, Appl
133	9	1.8	194	4	US-10-230-435-32	Sequence 32, Appl
134	9	1.8	194	4	US-10-230-438-32	Sequence 32, Appl
135	9	1.8	194	4	US-10-232-222-32	Sequence 32, Appl
136	9	1.8	194	4	US-10-219-070-32	Sequence 32, Appl
137	9	1.8	194	4	US-10-219-472-32	Sequence 32, Appl
138	9	1.8	194	4	US-10-219-527-32	Sequence 32, Appl
139	9	1.8	194	4	US-10-227-877-32	Sequence 32, Appl
140	9	1.8	194	4	US-10-216-166-32	Sequence 32, Appl
141	9	1.8	194	4	US-10-218-612-32	Sequence 32, Appl
142	9	1.8	194	4	US-10-216-163-32	Sequence 32, Appl
143	9	1.8	194	4	US-10-218-765-32	Sequence 32, Appl
144	9	1.8	194	4	US-10-219-063-32	Sequence 32, Appl
145	9	1.8	194	4	US-10-219-066-32	Sequence 32, Appl
146	9	1.8	194	4	US-10-219-067-32	Sequence 32, Appl
147	9	1.8	194	4	US-10-219-068-32	Sequence 32, Appl
148	9	1.8	194	4	US-10-219-069-32	Sequence 32, Appl
149	9	1.8	194	4	US-10-219-073-32	Sequence 32, Appl
150	9	1.8	194	4	US-10-219-475-32	Sequence 32, Appl

ALIGNMENTS

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RESULT 1
US-09-731-872-242
; Sequence 242, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean Baptiste
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Jobert, Severin
;  TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
;  FILE REFERENCE: 78.US3.REG
;  CURRENT APPLICATION NUMBER: US/09/731,872
;  CURRENT FILING DATE:  2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/169,629
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: US 60/187,470
;  PRIOR FILING DATE: 2000-03-06
;  NUMBER OF SEQ ID NOS: 482
;  SOFTWARE: Patent.pm
;
; SEQ ID NO 242
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -27..-1
US-09-731-872-242

  Query Match            100.0%;  Score 508;  DB 3;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
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Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
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Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
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Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
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Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
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RESULT 2
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; Sequence 139, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et. al.
;  TITLE OF INVENTION: 97 Human secreted proteins
;  FILE REFERENCE: PZ028P2
;  CURRENT APPLICATION NUMBER: US/09/948,783
;  CURRENT FILING DATE:  2001-09-10
;  PRIOR APPLICATION NUMBER: 60/231,846
;  PRIOR FILING DATE: 2000-09-11
;  PRIOR APPLICATION NUMBER: 09/892,877
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: 09/437,658
;  PRIOR FILING DATE: 1999-11-10
;  PRIOR APPLICATION NUMBER: PCT/US99/09847
;  PRIOR FILING DATE: 1999-05-06
;  PRIOR APPLICATION NUMBER: 60/085,093
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,094
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,105
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;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,180
;  PRIOR FILING DATE: 1998-05-12
;  PRIOR APPLICATION NUMBER: 60/085,927
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,906
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,924
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,922
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,921
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,923
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,925
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,928
;  PRIOR FILING DATE: 1998-05-18
;  PRIOR APPLICATION NUMBER: 60/085,920
;  PRIOR FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 465
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-948-783-139

  Query Match           100.0%;  Score 508;  DB 3;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
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Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
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Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
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Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
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Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
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Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
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Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
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Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
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Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 3
US-09-876-997-242
; Sequence 242, Application US/09876997
; Publication No. US20030152921A1
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean Baptiste
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Jobert, Severin
;  TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
;  FILE REFERENCE: 78.US4.CIP
;  CURRENT APPLICATION NUMBER: US/09/876,997
;  CURRENT FILING DATE:  2001-06-08
;  PRIOR APPLICATION NUMBER: US 09/731,872
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/187,470
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: US 60/169,629
;  PRIOR FILING DATE: 1999-12-08
;  NUMBER OF SEQ ID NOS: 482
;  SOFTWARE: Patent.pm
; SEQ ID NO 242
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -27..-1
US-09-876-997-242

  Query Match           100.0%;  Score 508;  DB 3;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
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Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 4
US-10-643-836-242
; Sequence 242, Application US/10643836
; Publication No. US20050096458A1
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean Baptiste
```

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;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Jobert, Severin
;  TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
;  FILE REFERENCE: 78.US3.REG
;  CURRENT APPLICATION NUMBER: US/10/643,836
;  CURRENT FILING DATE:  2003-08-19
;  PRIOR APPLICATION NUMBER: US/09/731,872
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/169,629
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: US 60/187,470
;  PRIOR FILING DATE: 2000-03-06
;  NUMBER OF SEQ ID NOS: 482
;  SOFTWARE: Patent.pm
; SEQ ID NO 242
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -27..-1
US-10-643-836-242

  Query Match           100.0%;  Score 508;  DB 5;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
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Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
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Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
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Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 5
US-10-472-533-371
; Sequence 371, Application US/10472533
; Publication No. US20050197285A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc.
;  TITLE OF INVENTION: Human Secreted Proteins
;  FILE REFERENCE: PS906PCT
;  CURRENT APPLICATION NUMBER: US/10/472,533
;  CURRENT FILING DATE:  2003-09-20
;  PRIOR APPLICATION NUMBER: US 60/331,287
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/306,171
;  PRIOR FILING DATE: 2001-07-19
;  PRIOR APPLICATION NUMBER: US 60/277,340
;  PRIOR FILING DATE: 2001-03-21
;  NUMBER OF SEQ ID NOS: 650
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 371
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-472-533-371

  Query Match           100.0%;  Score 508;  DB 5;  Length 508;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 6
US-09-892-877-137
; Sequence 137, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et. al.
;  TITLE OF INVENTION: 97 Human secreted proteins
;  FILE REFERENCE: PZ028P1
;  CURRENT APPLICATION NUMBER: US/09/892,877
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
;   LENGTH: 509
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (509)
;   OTHER INFORMATION: Xaa equals stop translation
US-09-892-877-137

  Query Match           100.0%;  Score 508;  DB 3;  Length 509;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  508;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 7
US-09-963-290-2
; Sequence 2, Application US/09963290
; Patent No. US20020137713A1
; GENERAL INFORMATION:
;  APPLICANT: Kapeller-Libermann, Rosana
;  TITLE OF INVENTION: 55054, A No. US20020137713A1el Human Metalloprotease and Uses The
;  FILE REFERENCE: 10147-47U1
;  CURRENT APPLICATION NUMBER: US/09/963,290
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: US 60/235,055
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-963-290-2

  Query Match           96.9%;  Score 492;  DB 3;  Length 507;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507


RESULT 8
US-09-931-836-57
; Sequence 57, Application US/09931836
; Publication No. US20030027249A1
; GENERAL INFORMATION:
;  APPLICANT: Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3030R1C1
;  CURRENT APPLICATION NUMBER: US/09/931,836
;  CURRENT FILING DATE:  2001-08-16
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/112514
;  PRIOR FILING DATE: 1998-12-15
;  PRIOR APPLICATION NUMBER: 60/113300
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: 60/113430
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113605
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/114140
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/115552
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116843
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; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131272
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-931-836-57

Query Match 96.9%; Score 492; DB 3; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507
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RESULT 9
US-10-036-342-57
; Sequence 57, Application US/10036342
; Publication No. US20020090681A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.

; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C5
; CURRENT APPLICATION NUMBER: US/10/036,342
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
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; PRIOR APPLICATION NUMBER: 60/129122
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
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; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-342-57

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
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Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
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Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
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Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
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Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
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Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507


RESULT 10
US-10-036-041-57
; Sequence 57, Application US/10036041
; Publication No. US20020192751A1
; GENERAL INFORMATION:
;  APPLICANT: Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3030R1C8
;  CURRENT APPLICATION NUMBER: US/10/036,041
;  CURRENT FILING DATE:  2001-12-26
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/112514
;  PRIOR FILING DATE: 1998-12-15
;  PRIOR APPLICATION NUMBER: 60/113300
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;  PRIOR APPLICATION NUMBER: 60/113430
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;  PRIOR APPLICATION NUMBER: 09/380142
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;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
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;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: PCT/US00/23522
;  PRIOR FILING DATE: 2000-08-23
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;  PRIOR FILING DATE: 2000-08-24
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;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 80
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; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-041-57

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
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Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
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Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
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Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
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Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
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Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507
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RESULT 11
US-10-035-855-57
; Sequence 57, Application US/10035855
; Publication No. US20030008348A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C4
; CURRENT APPLICATION NUMBER: US/10/035,855
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
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;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-035-855-57

  Query Match             96.9%;  Score 492;  DB 4;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
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Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
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Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
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Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
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Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
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Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
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Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507
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RESULT 12
US-10-036-214-57
; Sequence 57, Application US/10036214
; Publication No. US20030032061A1
; GENERAL INFORMATION:
;  APPLICANT: Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3030R1C11
;  CURRENT APPLICATION NUMBER: US/10/036,214
;  CURRENT FILING DATE:  2001-12-26
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/112514
;  PRIOR FILING DATE: 1998-12-15
;  PRIOR APPLICATION NUMBER: 60/113300
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: 60/113430
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113605
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/114140
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/115552
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116843
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/125774
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 60/125778
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 60/125826
;  PRIOR FILING DATE: 1999-03-24
;  PRIOR APPLICATION NUMBER: 60/127035
;  PRIOR FILING DATE: 1999-03-31
;  PRIOR APPLICATION NUMBER: 60/127706
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;  PRIOR APPLICATION NUMBER: 60/129122
;  PRIOR FILING DATE: 1999-04-13
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;  PRIOR FILING DATE: 1999-04-21
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;  PRIOR APPLICATION NUMBER: 60/135750
;  PRIOR FILING DATE: 1999-05-25
;  PRIOR APPLICATION NUMBER: 60/138166
;  PRIOR FILING DATE: 1999-06-08
;  PRIOR APPLICATION NUMBER: 60/144791
;  PRIOR FILING DATE: 1999-07-20
;  PRIOR APPLICATION NUMBER: 60/146970
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; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 2000-08-22
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; PRIOR FILING DATE: 2000-12-20
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; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-214-57

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
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Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
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Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
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Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
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Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
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Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
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Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507
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RESULT 13
US-10-035-719-57
; Sequence 57, Application US/10035719
; Publication No. US20030036114A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C2
; CURRENT APPLICATION NUMBER: US/10/035,719
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
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; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826

; PRIOR FILING DATE: 1999-03-24
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; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
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; PRIOR APPLICATION NUMBER: 60/146970
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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
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; PRIOR APPLICATION NUMBER: 09/747259
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; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
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; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
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; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-035-719-57

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
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Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
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Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
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Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
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Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
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Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507
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RESULT 14
US-10-036-160-57
; Sequence 57, Application US/10036160
; Publication No. US20030044842A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3030R1C3
; CURRENT APPLICATION NUMBER: US/10/036,160
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/113605
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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
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; PRIOR APPLICATION NUMBER: 60/125826
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; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
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; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
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; PRIOR APPLICATION NUMBER: PCT/US99/28551
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-036-160-57

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375
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Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507


RESULT 15
US-10-035-958-57
; Sequence 57, Application US/10035958
; Publication No. US20030049733A1
; GENERAL INFORMATION:
;  APPLICANT: Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3030R1C7
;  CURRENT APPLICATION NUMBER: US/10/035,958
;  CURRENT FILING DATE:  2001-12-26
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/112514
;  PRIOR FILING DATE: 1998-12-15
;  PRIOR APPLICATION NUMBER: 60/113300
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: 60/113430
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113605
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/114140
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/115552
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116843
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/125774
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 60/125778
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 60/125826
;  PRIOR FILING DATE: 1999-03-24
;  PRIOR APPLICATION NUMBER: 60/127035
;  PRIOR FILING DATE: 1999-03-31
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;  PRIOR FILING DATE: 1999-04-05
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;  PRIOR APPLICATION NUMBER: 60/130359
;  PRIOR FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: 60/131270
;  PRIOR FILING DATE: 1999-04-27
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;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131291
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;  PRIOR APPLICATION NUMBER: 60/132371
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/132379
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/132383
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/135750
;  PRIOR FILING DATE: 1999-05-25
;  PRIOR APPLICATION NUMBER: 60/138166
;  PRIOR FILING DATE: 1999-06-08
;  PRIOR APPLICATION NUMBER: 60/144791
;  PRIOR FILING DATE: 1999-07-20
;  PRIOR APPLICATION NUMBER: 60/146970
;  PRIOR FILING DATE: 1999-08-03
;  PRIOR APPLICATION NUMBER: 60/162506
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: 09/311832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: 09/380142
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/644848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 09/747259
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 09/816744
;  PRIOR FILING DATE: 2001-03-22
;  PRIOR APPLICATION NUMBER: 09/854208
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 09/854280
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 09/874503
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: 09/869599
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: 09/908,827
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US99/10733
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: PCT/US99/28551
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30720
;  PRIOR FILING DATE: 1999-12-22
;  PRIOR APPLICATION NUMBER: PCT/US00/05601
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: PCT/US00/23522
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US00/34956
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-035-958-57
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  Query Match           96.9%;  Score 492;  DB 4;  Length 507;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
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Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507


RESULT 16
US-10-036-150-57
; Sequence 57, Application US/10036150
; Publication No. US20030049734A1
; GENERAL INFORMATION:
;  APPLICANT: Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3030R1C9
;  CURRENT APPLICATION NUMBER: US/10/036,150
;  CURRENT FILING DATE:  2001-12-26
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/112514
;  PRIOR FILING DATE: 1998-12-15
;  PRIOR APPLICATION NUMBER: 60/113300
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: 60/113430
;  PRIOR FILING DATE: 1998-12-23
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;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/114140
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/115552
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116843
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/125774
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 60/125778
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 60/125826
;  PRIOR FILING DATE: 1999-03-24
;  PRIOR APPLICATION NUMBER: 60/127035
;  PRIOR FILING DATE: 1999-03-31
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;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: 60/129122
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;  PRIOR APPLICATION NUMBER: 60/130359
;  PRIOR FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: 60/131270
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131272
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/131291
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/132371
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/132379
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/132383
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/135750
;  PRIOR FILING DATE: 1999-05-25
;  PRIOR APPLICATION NUMBER: 60/138166
;  PRIOR FILING DATE: 1999-06-08
;  PRIOR APPLICATION NUMBER: 60/144791
;  PRIOR FILING DATE: 1999-07-20
;  PRIOR APPLICATION NUMBER: 60/146970
;  PRIOR FILING DATE: 1999-08-03
;  PRIOR APPLICATION NUMBER: 60/162506
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: 09/311832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: 09/380142
;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/644848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 09/747259
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 09/816744
;  PRIOR FILING DATE: 2001-03-22
;  PRIOR APPLICATION NUMBER: 09/854208
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 09/854280
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 09/874503
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: 09/869599
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: 09/908,827
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US99/10733
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: PCT/US99/28551
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30720
;  PRIOR FILING DATE: 1999-12-22
;  PRIOR APPLICATION NUMBER: PCT/US00/05601
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
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;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: PCT/US00/23522
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US00/34956
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-036-150-57

  Query Match             96.9%;  Score 492;  DB 4;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507


RESULT 17
US-10-036-063-57
; Sequence 57, Application US/10036063
; Publication No. US20030092063A1
; GENERAL INFORMATION:
;  APPLICANT: Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3030R1C6
;  CURRENT APPLICATION NUMBER: US/10/036,063
;  CURRENT FILING DATE:  2001-12-26
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/112514
;  PRIOR FILING DATE: 1998-12-15
;  PRIOR APPLICATION NUMBER: 60/113300
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: 60/113430
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113605
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/114140
;  PRIOR FILING DATE: 1998-12-23
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;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116843
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;  PRIOR APPLICATION NUMBER: 60/127035
;  PRIOR FILING DATE: 1999-03-31
;  PRIOR APPLICATION NUMBER: 60/127706
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;  PRIOR APPLICATION NUMBER: 60/129122
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;  PRIOR APPLICATION NUMBER: 60/131291
;  PRIOR FILING DATE: 1999-04-27
;  PRIOR APPLICATION NUMBER: 60/132371
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/132379
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/132383
;  PRIOR FILING DATE: 1999-05-04
;  PRIOR APPLICATION NUMBER: 60/135750
;  PRIOR FILING DATE: 1999-05-25
;  PRIOR APPLICATION NUMBER: 60/138166
;  PRIOR FILING DATE: 1999-06-08
;  PRIOR APPLICATION NUMBER: 60/144791
;  PRIOR FILING DATE: 1999-07-20
;  PRIOR APPLICATION NUMBER: 60/146970
;  PRIOR FILING DATE: 1999-08-03
;  PRIOR APPLICATION NUMBER: 60/162506
;  PRIOR FILING DATE: 1999-10-29
;  PRIOR APPLICATION NUMBER: 09/311832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: 09/380142
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;  PRIOR FILING DATE: 1999-08-25
;  PRIOR APPLICATION NUMBER: 09/644848
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 09/747259
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 09/816744
;  PRIOR FILING DATE: 2001-03-22
;  PRIOR APPLICATION NUMBER: 09/854208
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 09/854280
;  PRIOR FILING DATE: 2001-05-10
;  PRIOR APPLICATION NUMBER: 09/874503
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: 09/869599
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: 09/908,827
;  PRIOR FILING DATE: 2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US99/10733
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: PCT/US99/28551
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30720
;  PRIOR FILING DATE: 1999-12-22
;  PRIOR APPLICATION NUMBER: PCT/US00/05601
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: PCT/US00/05841
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US00/15264
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: PCT/US00/23522
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: 2000-12-01
;  PRIOR APPLICATION NUMBER: PCT/US00/34956
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: PCT/US01/17800
;  PRIOR FILING DATE: 2001-06-01
;  PRIOR APPLICATION NUMBER: PCT/US01/19692
;  PRIOR FILING DATE: 2001-06-20
;  PRIOR APPLICATION NUMBER: PCT/US01/21066
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: PCT/US01/21735
;  PRIOR FILING DATE: 2001-07-09
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-036-063-57

  Query Match             96.9%;  Score 492;  DB 4;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
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Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
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Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
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Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507


RESULT 18
US-10-035-977-57
; Sequence 57, Application US/10035977
; Publication No. US20030134327A1
; GENERAL INFORMATION:
;  APPLICANT: Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3030R1C10
;  CURRENT APPLICATION NUMBER: US/10/035,977
;  CURRENT FILING DATE:  2001-12-26
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/112514
;  PRIOR FILING DATE: 1998-12-15
;  PRIOR APPLICATION NUMBER: 60/113300
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: 60/113430
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113605
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/114140
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/115552
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116843
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/125774
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 60/125778
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 60/125826
;  PRIOR FILING DATE: 1999-03-24
;  PRIOR APPLICATION NUMBER: 60/127035
;  PRIOR FILING DATE: 1999-03-31
;  PRIOR APPLICATION NUMBER: 60/127706
;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: 60/129122
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; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
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; PRIOR FILING DATE: 1999-05-04
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; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
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; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
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; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-035-977-57

Query Match 96.9%; Score 492; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
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Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
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Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507
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RESULT 19
US-10-275-107-68
; Sequence 68, Application US/10275107
; Publication No. US20040063107A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN R.
; APPLICANT: PAYNE, VILLA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1479
; CURRENT APPLICATION NUMBER: US/10/275,107
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/US01/14431
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/201,879
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 68
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-275-107-68

  Query Match            96.9%;  Score 492;  DB 4;  Length 507;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
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Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
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Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

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Db        196 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 255

Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
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Db        256 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 315

Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
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Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Db        376 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 435

Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
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Db        496 FAAFFLEMAQLH 507


RESULT 20
US-10-884-091-57
; Sequence 57, Application US/10884091
; Publication No. US20040265966A1
; GENERAL INFORMATION:
;  APPLICANT: Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODIN
;  TITLE OF INVENTION:  THE SAME
;  FILE REFERENCE: P3030R1C1C1
;  CURRENT APPLICATION NUMBER: US/10/884,091
;  CURRENT FILING DATE:  2004-07-01
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/112514
;  PRIOR FILING DATE: 1998-12-15
;  PRIOR APPLICATION NUMBER: 60/113300
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: 60/113430
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113605
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/113621
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/114140
;  PRIOR FILING DATE: 1998-12-23
;  PRIOR APPLICATION NUMBER: 60/115552
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/116843
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/125774
;  PRIOR FILING DATE: 1999-03-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 57
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-884-091-57

  Query Match            96.9%;  Score 492;  DB 5;  Length 507;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  492;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 76
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Db         16 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELF 75

Qy         77 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 136
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Db         76 RMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDV 135

Qy        137 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 196
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Db        136 QPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFII 195

Qy        197 EGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKC 256
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Qy        257 RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL 316
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Qy        317 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 376
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Db        316 DLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSI 375

Qy        377 RLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIR 436
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Qy        437 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 496
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Db        436 TVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKL 495

Qy        497 FAAFFLEMAQLH 508
              ||||||||||||
Db        496 FAAFFLEMAQLH 507


RESULT 21
US-09-791-378-674
; Sequence 674, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
;  APPLICANT: Parekh, Rajesh
;  TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
;  TITLE OF INVENTION:  SCHIZOPHRENIA
;  FILE REFERENCE: 9195-061-999
;  CURRENT APPLICATION NUMBER: US/09/791,378
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;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/750,395
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 677
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 674
;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (70)..(70)
;   OTHER INFORMATION: Xaa = Ile or Leu
US-09-791-378-674

  Query Match             84.4%;  Score 429;  DB 3;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 130

Qy        138 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 190

Qy        198 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250

Qy        258 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310

Qy        318 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370

Qy        378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 430

Qy        438 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490

Qy        498 AAFFLEMAQ 506
              |||||||||
Db        491 AAFFLEMAQ 499


RESULT 22
US-09-791-393-2
; Sequence 2, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
;  APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
;  APPLICANT: Parekh, Rajesh Bhikhu
;  APPLICANT: Rohlff, Christian
;  TITLE OF INVENTION: Proteins, Genes and Their Use for
;  TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
;  TITLE OF INVENTION: and Unipolar Depression
;  FILE REFERENCE: 2543-1-001 N1
;  CURRENT APPLICATION NUMBER: US/09/791,393
;  CURRENT FILING DATE: 2002-01-02
;  EARLIER APPLICATION NUMBER: GB 0004412.3
;  EARLIER FILING DATE: 2000-02-24
;  EARLIER APPLICATION NUMBER: GB 0030050.9
;  EARLIER FILING DATE: 2000-12-08
;  EARLIER APPLICATION NUMBER: US 60/254,830
;  EARLIER FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 308
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: homo sapien
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(501)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-791-393-2

  Query Match             84.4%;  Score 429;  DB 3;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 130

Qy        138 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 190

Qy        198 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250

Qy        258 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310

Qy        318 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370

Qy        378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 430

Qy        438 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490

Qy        498 AAFFLEMAQ 506
              |||||||||
Db        491 AAFFLEMAQ 499


RESULT 23
US-09-791-389-2
; Sequence 2, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
;  APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
;  APPLICANT:  Parekh, Rajesh Bhikhu
;  APPLICANT:  Rohlff, Christian
;  APPLICANT:  Terrett, Jonathan Alexander
;  APPLICANT:  Tyson, Kerry Louise
;  TITLE OF INVENTION: Proteins, Genes and Their Use for
;  TITLE OF INVENTION:  Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
;  TITLE OF INVENTION:  and Unipolar Depression
;  FILE REFERENCE: 2543-1-001 N2
;  CURRENT APPLICATION NUMBER: US/09/791,389
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: GB 0004412.3
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: GB 0030050.9
;  PRIOR FILING DATE: 2000-12-08
;  PRIOR APPLICATION NUMBER: US 60/254,830
;  PRIOR FILING DATE: 2000-12-12
;  NUMBER OF SEQ ID NOS: 308
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
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;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: homo sapien
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(501)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-791-389-2

  Query Match           84.4%;  Score 429;  DB 3;  Length 501;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 130

Qy        138 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 190

Qy        198 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250

Qy        258 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310

Qy        318 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370

Qy        378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 430

Qy        438 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490

Qy        498 AAFFLEMAQ 506
              |||||||||
Db        491 AAFFLEMAQ 499


RESULT 24
US-09-791-377-674
; Sequence 674, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
;  APPLICANT: Parekh, Rajesh
;  TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
;  TITLE OF INVENTION:  SCHIZOPHRENIA
;  FILE REFERENCE: 9195-060-999
;  CURRENT APPLICATION NUMBER: US/09/791,377
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/750,395
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 677
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 674
;   LENGTH: 501
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (70)..(70)
;   OTHER INFORMATION: Xaa = Ile or Leu
US-09-791-377-674

  Query Match           84.4%;  Score 429;  DB 3;  Length 501;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  429;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         78 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 MMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQ 130

Qy        138 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 PADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIE 190

Qy        198 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCR 250

Qy        258 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 DQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLD 310

Qy        318 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIR 370

Qy        378 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 LVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRT 430

Qy        438 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        431 VFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF 490

Qy        498 AAFFLEMAQ 506
              |||||||||
Db        491 AAFFLEMAQ 499


RESULT 25
US-10-369-022-54
; Sequence 54, Application US/10369022
; Publication No. US20030203847A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Rosenfeld, Julie Beth
;  APPLICANT:  Silos-Santiago, Inmaculada
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
;  TITLE OF INVENTION:  PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
;  TITLE OF INVENTION:  12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
;  TITLE OF INVENTION:  27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
;  TITLE OF INVENTION:  95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
;  TITLE OF INVENTION:  13424 MOLECULES
;  FILE REFERENCE: MPI02-027P1RNOMNIM
;  CURRENT APPLICATION NUMBER: US/10/369,022
;  CURRENT FILING DATE:  2003-02-19
;  PRIOR APPLICATION NUMBER: US 60/360,495
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/370,121
;  PRIOR FILING DATE: 2002-04-04
;  PRIOR APPLICATION NUMBER: US 60/373,010
;  PRIOR FILING DATE: 2002-04-16
;  PRIOR APPLICATION NUMBER: US 60/373,908
;  PRIOR FILING DATE: 2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/377,717
;  PRIOR FILING DATE: 2002-05-03
;  PRIOR APPLICATION NUMBER: US 60/379,949
;  PRIOR FILING DATE: 2002-05-13
;  PRIOR APPLICATION NUMBER: US 60/382,409
;  PRIOR FILING DATE: 2002-05-21
;  PRIOR APPLICATION NUMBER: US 60/385,280
;  PRIOR FILING DATE: 2002-06-03
;  PRIOR APPLICATION NUMBER: US 60/386,879
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/387,536
;  PRIOR FILING DATE: 2002-06-10
;  Remaining Prior Application data removed - See File Wrapper or PALM.
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;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-369-022-54

  Query Match             46.3%;  Score 235;  DB 4;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-212;
  Matches  235;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        274 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFD 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFD 333

Qy        334 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 TKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTR 393

Qy        394 HLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 HLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIP 453

Qy        454 IAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 IAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 26
US-10-296-115-1427
; Sequence 1427, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq Inc
;  TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 784PCT
;  CURRENT APPLICATION NUMBER: US/10/296,115
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: US09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1427
;   LENGTH: 133
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-296-115-1427

  Query Match             24.8%;  Score 126;  DB 4;  Length 133;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-110;
  Matches  126;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 67

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 127

Qy        121 SDPTKG 126
              ||||||
Db        128 SDPTKG 133


RESULT 27
US-10-264-237-2057
; Sequence 2057, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA131P1
;  CURRENT APPLICATION NUMBER: US/10/264,237
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: PCT/US01/16450
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 60/205,515
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 2876
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2057
;   LENGTH: 316
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-264-237-2057

  Query Match             19.7%;  Score 100;  DB 4;  Length 316;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-85;
  Matches  100;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        212 EKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILH 271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 EKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILH 248

Qy        272 EPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY 311
              |||||||||||||||||||||||||||||||||||||||||
Db        249 EPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY 288


RESULT 28
US-10-450-763-32013
; Sequence 32013, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 32013
;   LENGTH: 100
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(100)
;   OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-32013

  Query Match             10.6%;  Score 54;  DB 5;  Length 100;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-42;
  Matches   54;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIE 54


RESULT 29
US-10-450-763-32012
; Sequence 32012, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
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;  FILE REFERENCE: 790CIP3/US
;  CURRENT APPLICATION NUMBER: US/10/450,763
;  CURRENT FILING DATE:  2003-06-11
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  NUMBER OF SEQ ID NOS: 60736
;  SOFTWARE: Custom
; SEQ ID NO 32012
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-450-763-32012

  Query Match             7.3%;  Score 37;  DB 5;  Length 157;
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Db         62 LLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQT 98


RESULT 30
US-09-791-378-199
; Sequence 199, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
;  APPLICANT: Parekh, Rajesh
;  TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
;  TITLE OF INVENTION:  SCHIZOPHRENIA
;  FILE REFERENCE: 9195-061-999
;  CURRENT APPLICATION NUMBER: US/09/791,378
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: 09/750,395
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 677
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 199
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-378-199

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Db          1 EWVAIESDSVQPVPR 15


Search completed: March 30, 2006, 09:16:19
Job time : 172 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 30, 2006, 09:13:38 ; Search time 24 Seconds
(without alignments)
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Title: US-10-849-979-139
Perfect score: 508
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 180808 seqs, 30441898 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1532

Minimum DB seq length: 0
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Post-processing: Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9	1.8	209	6	US-10-467-657-4066	Sequence 4066, Ap
2	9	1.8	475	6	US-10-878-556A-115	Sequence 115, App
3	9	1.8	497	7	US-11-087-099-5884	Sequence 5884, Ap
4	8	1.6	78	7	US-11-123-896-278	Sequence 278, App
5	8	1.6	82	7	US-11-123-896-56	Sequence 56, Appl
6	8	1.6	110	7	US-11-087-099-8542	Sequence 8542, Ap
7	8	1.6	114	7	US-11-087-099-2900	Sequence 2900, Ap
8	8	1.6	277	7	US-11-140-416-34	Sequence 34, Appl
9	8	1.6	293	7	US-11-096-568A-12504	Sequence 12504, A
10	8	1.6	578	7	US-11-037-243-100	Sequence 100, App
11	8	1.6	579	7	US-11-096-568A-20038	Sequence 20038, A
12	8	1.6	852	6	US-10-645-441-15	Sequence 15, Appl
13	8	1.6	852	6	US-10-725-475-7	Sequence 7, Appli
14	8	1.6	852	7	US-11-050-804-6	Sequence 6, Appli
15	8	1.6	999	7	US-11-113-424-36	Sequence 36, Appl
16	7	1.4	36	6	US-10-517-696-137	Sequence 137, App
17	7	1.4	79	7	US-11-123-896-468	Sequence 468, App
18	7	1.4	86	6	US-10-475-075-175	Sequence 175, App
19	7	1.4	86	6	US-10-475-075-460	Sequence 460, App
20	7	1.4	86	7	US-11-096-568A-13143	Sequence 13143, A
21	7	1.4	99	7	US-11-176-951-11	Sequence 11, Appl
22	7	1.4	101	6	US-10-485-788A-775	Sequence 775, App
23	7	1.4	101	7	US-11-053-076-157	Sequence 157, App
24	7	1.4	129	6	US-10-475-075-242	Sequence 242, App
25	7	1.4	129	6	US-10-475-075-243	Sequence 243, App
26	7	1.4	129	6	US-10-475-075-513	Sequence 513, App
27	7	1.4	133	6	US-10-644-807-297	Sequence 297, App
28	7	1.4	154	7	US-11-096-568A-13303	Sequence 13303, A
29	7	1.4	160	7	US-11-096-568A-22510	Sequence 22510, A
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33	7	1.4	190	6	US-10-973-115B-158	Sequence 158, App
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38	7	1.4	242	6	US-10-063-703-136	Sequence 136, App
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40	7	1.4	242	7	US-11-080-991-30	Sequence 30, Appl
41	7	1.4	242	7	US-11-103-195-136	Sequence 136, App
42	7	1.4	253	6	US-10-821-234-865	Sequence 865, App
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47	7	1.4	295	7	US-11-096-568A-18354	Sequence 18354, A
48	7	1.4	297	7	US-11-096-568A-18353	Sequence 18353, A
49	7	1.4	301	6	US-10-055-877-124	Sequence 124, App
50	7	1.4	301	6	US-10-055-877-261	Sequence 261, App
51	7	1.4	301	7	US-11-000-463-280	Sequence 280, App
52	7	1.4	301	7	US-11-000-463-752	Sequence 752, App
53	7	1.4	301	7	US-11-087-177-35	Sequence 35, Appl
54	7	1.4	301	7	US-11-087-177-37	Sequence 37, Appl
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56	7	1.4	320	7	US-11-150-758-2	Sequence 2, Appli
57	7	1.4	328	6	US-10-131-826A-364	Sequence 364, App
58	7	1.4	328	6	US-10-973-115B-364	Sequence 364, App
59	7	1.4	329	7	US-11-096-568A-5471	Sequence 5471, Ap
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61	7	1.4	330	7	US-11-087-099-612	Sequence 612, App
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66	7	1.4	346	7	US-11-172-740-1221	Sequence 1221, Ap
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70	7	1.4	359	7	US-11-055-822-842	Sequence 842, App
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73	7	1.4	377	7	US-11-096-568A-12688	Sequence 12688, A
74	7	1.4	381	7	US-11-096-568A-12687	Sequence 12687, A
75	7	1.4	401	6	US-10-055-877-77	Sequence 77, Appl
76	7	1.4	413	7	US-11-096-568A-20771	Sequence 20771, A
77	7	1.4	419	7	US-11-172-740-744	Sequence 744, App
78	7	1.4	429	7	US-11-087-099-5975	Sequence 5975, Ap
79	7	1.4	446	7	US-11-096-568A-20810	Sequence 20810, A
80	7	1.4	457	7	US-11-096-568A-20809	Sequence 20809, A
81	7	1.4	461	6	US-10-509-464-7	Sequence 7, Appli
82	7	1.4	465	7	US-11-087-099-8829	Sequence 8829, Ap
83	7	1.4	469	7	US-11-096-568A-6976	Sequence 6976, Ap
84	7	1.4	475	6	US-10-509-464-8	Sequence 8, Appli
85	7	1.4	510	7	US-11-194-246-442	Sequence 442, App
86	7	1.4	526	6	US-10-467-657-6754	Sequence 6754, Ap
87	7	1.4	534	7	US-11-096-568A-14686	Sequence 14686, A
88	7	1.4	544	7	US-11-087-099-5596	Sequence 5596, Ap
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90	7	1.4	569	7	US-11-096-568A-6975	Sequence 6975, Ap
91	7	1.4	597	6	US-10-884-730-381	Sequence 381, App
92	7	1.4	598	7	US-11-096-568A-6974	Sequence 6974, Ap
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94	7	1.4	615	7	US-11-198-819-18	Sequence 18, Appl
95	7	1.4	642	6	US-10-131-826A-370	Sequence 370, App
96	7	1.4	642	6	US-10-973-115B-370	Sequence 370, App
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102	7	1.4	857	7	US-11-096-568A-24558	Sequence 24558, A
103	7	1.4	858	7	US-11-087-099-11449	Sequence 11449, A
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109	7	1.4	1857	6	US-10-055-877-252	Sequence 252, App
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111	7	1.4	2107	6	US-10-995-561-827	Sequence 827, App
112	7	1.4	2109	6	US-10-055-877-251	Sequence 251, App
113	7	1.4	2186	7	US-11-096-568A-28283	Sequence 28283, A
114	7	1.4	2199	7	US-11-096-568A-28282	Sequence 28282, A
115	7	1.4	2301	7	US-11-096-568A-28281	Sequence 28281, A
116	7	1.4	2480	6	US-10-995-561-825	Sequence 825, App
117	7	1.4	3116	6	US-10-995-561-826	Sequence 826, App
118	6	1.2	8	7	US-11-045-024-1669	Sequence 1669, Ap
119	6	1.2	8	7	US-11-045-024-9615	Sequence 9615, Ap
120	6	1.2	9	7	US-11-045-024-1881	Sequence 1881, Ap
121	6	1.2	9	7	US-11-045-024-5335	Sequence 5335, Ap
122	6	1.2	9	7	US-11-045-024-9622	Sequence 9622, Ap
123	6	1.2	9	7	US-11-033-039-883	Sequence 883, App
124	6	1.2	10	7	US-11-045-024-2105	Sequence 2105, Ap
125	6	1.2	10	7	US-11-045-024-4631	Sequence 4631, Ap
126	6	1.2	10	7	US-11-045-024-9629	Sequence 9629, Ap
127	6	1.2	10	7	US-11-254-419-29	Sequence 29, Appl
128	6	1.2	11	7	US-11-045-024-2326	Sequence 2326, Ap
129	6	1.2	11	7	US-11-045-024-2328	Sequence 2328, Ap
130	6	1.2	11	7	US-11-045-024-4784	Sequence 4784, Ap
131	6	1.2	11	7	US-11-045-024-5399	Sequence 5399, Ap
132	6	1.2	11	7	US-11-045-024-9643	Sequence 9643, Ap
133	6	1.2	12	6	US-10-989-226-17	Sequence 17, Appl
134	6	1.2	12	7	US-11-066-967-44	Sequence 44, Appl
135	6	1.2	15	6	US-10-431-638-6	Sequence 6, Appli
136	6	1.2	15	6	US-10-513-465-6	Sequence 6, Appli
137	6	1.2	15	7	US-11-045-024-13266	Sequence 13266, A
138	6	1.2	15	7	US-11-045-024-13428	Sequence 13428, A
139	6	1.2	16	7	US-11-197-488-21	Sequence 21, Appl
140	6	1.2	17	6	US-10-967-457-34	Sequence 34, Appl
141	6	1.2	17	7	US-11-078-663-34	Sequence 34, Appl
142	6	1.2	17	7	US-11-078-914-34	Sequence 34, Appl
143	6	1.2	17	7	US-11-033-039-896	Sequence 896, App
144	6	1.2	17	7	US-11-221-849-6	Sequence 6, Appli
145	6	1.2	17	7	US-11-175-690-7	Sequence 7, Appli
146	6	1.2	18	6	US-10-498-665-79	Sequence 79, Appl
147	6	1.2	18	6	US-10-498-665-81	Sequence 81, Appl
148	6	1.2	19	6	US-10-503-575-205	Sequence 205, App
149	6	1.2	20	6	US-10-623-155-553	Sequence 553, App
150	6	1.2	20	6	US-10-623-155-554	Sequence 554, App

ALIGNMENTS

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RESULT 1
US-10-467-657-4066
; Sequence 4066, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4066
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4066

  Query Match             1.8%;  Score 9;  DB 6;  Length 209;
  Best Local Similarity   100.0%;  Pred. No. 0.78;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 LLAVLLLLL 20
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Db        165 LLAVLLLLL 173


RESULT 2
US-10-878-556A-115
; Sequence 115, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
;  APPLICANT: Hoffmann La-Roche Inc.
;  TITLE OF INVENTION: HCV regulated protein expression
;  FILE REFERENCE: 21762
;  CURRENT APPLICATION NUMBER: US/10/878,556A
;  CURRENT FILING DATE:  2004-06-28
;  NUMBER OF SEQ ID NOS: 199
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 115
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: sw_hum/cgl1_human
;   DATABASE ENTRY DATE: 2003-02-28
US-10-878-556A-115

  Query Match             1.8%;  Score 9;  DB 6;  Length 475;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        131 YGHLDVQPA 139
              |||||||||
Db         97 YGHLDVQPA 105


RESULT 3
US-11-087-099-5884
; Sequence 5884, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5884
;   LENGTH: 497
;   TYPE: PRT
;   ORGANISM: Yarrowia lipolytica
US-11-087-099-5884

  Query Match             1.8%;  Score 9;  DB 7;  Length 497;
  Best Local Similarity   100.0%;  Pred. No. 1.8;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 LLAVLLLLL 20
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Db        349 LLAVLLLLL 357
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RESULT 4
US-11-123-896-278
; Sequence 278, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-123-896-278

Query Match 1.6%; Score 8; DB 7; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
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Db 10 AVLLLLLL 17

RESULT 5
US-11-123-896-56
; Sequence 56, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-123-896-56

Query Match 1.6%; Score 8; DB 7; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
||||||||
Db 12 AVLLLLLL 19

RESULT 6
US-11-087-099-8542
; Sequence 8542, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8542
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-087-099-8542

Query Match 1.6%; Score 8; DB 7; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLAVLLLL 19
||||||||
Db 11 LLAVLLLL 18

RESULT 7
US-11-087-099-2900
; Sequence 2900, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2900
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-087-099-2900

Query Match 1.6%; Score 8; DB 7; Length 114;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLAVLLLL 19
||||||||
Db 13 LLAVLLLL 20

RESULT 8
US-11-140-416-34
; Sequence 34, Application US/11140416
; Publication No. US20060029547A1
; GENERAL INFORMATION:
; APPLICANT: D-Gen Limited
; TITLE OF INVENTION: BIOLOGICAL MATERIALS AND METHODS USEFUL IN THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PRION DISEASE
; FILE REFERENCE: ICOT/P21952
; CURRENT APPLICATION NUMBER: US/11/140,416
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: GB 9824091.4
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34

; LENGTH: 277
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-140-416-34

Query Match 1.6%; Score 8; DB 7; Length 277;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAVLLLLL 20
||||||||
Db 263 LAVLLLLL 270

RESULT 9
US-11-096-568A-12504
; Sequence 12504, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12504
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(293)
; OTHER INFORMATION: Ceres Seq. ID no. 14301931
US-11-096-568A-12504

Query Match 1.6%; Score 8; DB 7; Length 293;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 SSPSPPPA 34
||||||||
Db 97 SSPSPPPA 104

RESULT 10
US-11-037-243-100
; Sequence 100, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-100

Query Match 1.6%; Score 8; DB 7; Length 578;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLAVLLLL 19
||||||||
Db 2 LLAVLLLL 9

RESULT 11
US-11-096-568A-20038
; Sequence 20038, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20038
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(579)
; OTHER INFORMATION: Ceres Seq. ID no. 12376563
US-11-096-568A-20038

Query Match 1.6%; Score 8; DB 7; Length 579;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAVLLLLL 20
||||||||
Db 17 LAVLLLLL 24

RESULT 12
US-10-645-441-15
; Sequence 15, Application US/10645441
; Publication No. US20050260599A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J.P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrashekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02307E-120110US
; CURRENT APPLICATION NUMBER: US/10/645,441
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US/09/927,315
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human T1R3 sweet taste receptor
US-10-645-441-15

Query Match 1.6%; Score 8; DB 6; Length 852;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         14 AVLLLLLL 21
              ||||||||
Db        568 AVLLLLLL 575
```

RESULT 13
US-10-725-475-7
; Sequence 7, Application US/10725475
; Publication No. US20060014208A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG
; APPLICANT: ECHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
; FILE REFERENCE: 078003-0291566
; CURRENT APPLICATION NUMBER: US/10/725,475
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/300,434
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/304,749
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/310,493
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/331,771
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/339,472
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/372,090
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/374,143
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-725-475-7

Query Match 1.6%; Score 8; DB 6; Length 852;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         14 AVLLLLLL 21
              ||||||||
Db        568 AVLLLLLL 575
```

RESULT 14
US-11-050-804-6
; Sequence 6, Application US/11050804
; Publication No. US20050287517A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: LI, XIADONG
; APPLICANT: STAZEWSKI, LENA
; APPLICANT: XU, HONG
; APPLICANT: EHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS
; FILE REFERENCE: T1530-00006
; CURRENT APPLICATION NUMBER: US/11/050,804
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: 09/897,427
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/284,547
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 60/300,434
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-804-6

Query Match 1.6%; Score 8; DB 7; Length 852;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         14 AVLLLLLL 21
              ||||||||
Db        568 AVLLLLLL 575
```

RESULT 15
US-11-113-424-36
; Sequence 36, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 999
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-36

Query Match 1.6%; Score 8; DB 7; Length 999;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         14 AVLLLLLL 21
              ||||||||
Db         14 AVLLLLLL 21
```

RESULT 16
US-10-517-696-137
; Sequence 137, Application US/10517696
; Publication No. US20060051759A1
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.

; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto A.
; APPLICANT: Turner, Leah R.
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0432
; CURRENT APPLICATION NUMBER: US/10/517,696
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US 60/389,327
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 171
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-517-696-137

Query Match 1.4%; Score 7; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LLLLLLE 22
|||||||
Db 3 LLLLLLE 9

RESULT 17
US-11-123-896-468
; Sequence 468, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/300,241
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 468
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Zea mays
US-11-123-896-468

Query Match 1.4%; Score 7; DB 7; Length 79;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLL 20
|||||||
Db 13 AVLLLLL 19

RESULT 18
US-10-475-075-175
; Sequence 175, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 175
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18..-1
US-10-475-075-175

Query Match 1.4%; Score 7; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VLLLLLL 21
|||||||
Db 6 VLLLLLL 12

RESULT 19
US-10-475-075-460
; Sequence 460, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
; FILE REFERENCE: G-081US03PCT
; CURRENT APPLICATION NUMBER: US/10/475,075
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/IB01/00914
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 918
; SOFTWARE: Patent.pm
; SEQ ID NO 460
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -18..-1
US-10-475-075-460

Query Match 1.4%; Score 7; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 VLLLLLL 21
|||||||
Db 6 VLLLLLL 12

RESULT 20
US-11-096-568A-13143
; Sequence 13143, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I

```
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13143
;   LENGTH: 86
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(86)
;   OTHER INFORMATION: Ceres Seq. ID no. 15172623
US-11-096-568A-13143

  Query Match             1.4%;  Score 7;  DB 7;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 LLAVLLL 18
               |||||||
Db         11 LLAVLLL 17


RESULT 21
US-11-176-951-11
; Sequence 11, Application US/11176951
; Publication No. US20060024313A1
; GENERAL INFORMATION:
;  APPLICANT: CHEN, XIN
;  APPLICANT:  CHEN, YUAN-SHOU
;  TITLE OF INVENTION: AGENTS THAT DISRUPT DIMER FORMATION IN DPP-IV FAMILY OF
;  TITLE OF INVENTION:  PROLYL DIPEPTIDASES
;  FILE REFERENCE: 08842.0019
;  CURRENT APPLICATION NUMBER: US/11/176,951
;  CURRENT FILING DATE:  2005-07-06
;  PRIOR APPLICATION NUMBER: 60/586,095
;  PRIOR FILING DATE: 2004-07-06
;  PRIOR APPLICATION NUMBER: 60/585,952
;  PRIOR FILING DATE: 2004-07-06
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
;   LENGTH: 99
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-176-951-11

  Query Match             1.4%;  Score 7;  DB 7;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        201 EAGSVAL 207
              |||||||
Db         18 EAGSVAL 24


RESULT 22
US-10-485-788A-775
; Sequence 775, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Rabinowitz, Joshua D.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Carrick, Deanna Marie
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: Molecular Interactions in Cells
;  FILE REFERENCE: 20054-003320US
;  CURRENT APPLICATION NUMBER: US/10/485,788A
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: WO PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 775
;   LENGTH: 101
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-485-788A-775

  Query Match             1.4%;  Score 7;  DB 6;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        303 LTEEEIN 309
              |||||||
Db          2 LTEEEIN 8


RESULT 23
US-11-053-076-157
; Sequence 157, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Somoza Diaz-Sarmiento, Chamorro
;  APPLICANT:  Belmares, Michael P.
;  TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
;  FILE REFERENCE: VITA-008CIP
;  CURRENT APPLICATION NUMBER: US/11/053,076
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: PCT/US03/28508
;  PRIOR FILING DATE: 2003-09-09
;  PRIOR APPLICATION NUMBER: 10/630,590
;  PRIOR FILING DATE: 2003-07-29
;  PRIOR APPLICATION NUMBER: 60/490,094
;  PRIOR FILING DATE: 2003-07-25
;  PRIOR APPLICATION NUMBER: 60/450,464
;  PRIOR FILING DATE: 2003-02-27
;  PRIOR APPLICATION NUMBER: 60/409,298
;  PRIOR FILING DATE: 2002-09-09
;  PRIOR APPLICATION NUMBER: 10/630,590
;  PRIOR FILING DATE: 2003-07-29
;  PRIOR APPLICATION NUMBER: PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  PRIOR APPLICATION NUMBER: 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: 10/080,273
;  PRIOR FILING DATE: 2002-02-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 330
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 157
;   LENGTH: 101
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-053-076-157

  Query Match             1.4%;  Score 7;  DB 7;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        303 LTEEEIN 309
              |||||||
Db          2 LTEEEIN 8


RESULT 24
```

```
US-10-475-075-242
; Sequence 242, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
;  APPLICANT: Bejanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  APPLICANT:  Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT:  Jobert, Severin
;  APPLICANT:  Giordano, Jean-Yves
;  TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
;  FILE REFERENCE: G-081US03PCT
;  CURRENT APPLICATION NUMBER: US/10/475,075
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: PCT/IB01/00914
;  PRIOR FILING DATE: 2001-04-18
;  NUMBER OF SEQ ID NOS: 918
;  SOFTWARE: Patent.pm
; SEQ ID NO 242
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -16..-1
;   OTHER INFORMATION: Von Heijne matrix
;   OTHER INFORMATION: score 3.61791418904325
;   OTHER INFORMATION: seq LLLLLRALRRGPG/PG
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 84
;   OTHER INFORMATION: Xaa = Phe or Tyr
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 92
;   OTHER INFORMATION: Xaa = Gln or His
US-10-475-075-242

  Query Match             1.4%;  Score 7;  DB 6;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AVLLLLL 20
              |||||||
Db          2 AVLLLLL 8


RESULT 25
US-10-475-075-243
; Sequence 243, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
;  APPLICANT: Bejanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  APPLICANT:  Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT:  Jobert, Severin
;  APPLICANT:  Giordano, Jean-Yves
;  TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
;  FILE REFERENCE: G-081US03PCT
;  CURRENT APPLICATION NUMBER: US/10/475,075
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: PCT/IB01/00914
;  PRIOR FILING DATE: 2001-04-18
;  NUMBER OF SEQ ID NOS: 918
;  SOFTWARE: Patent.pm
; SEQ ID NO 243
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -16..-1
;   OTHER INFORMATION: Von Heijne matrix
;   OTHER INFORMATION: score 3.61791418904325
;   OTHER INFORMATION: seq LLLLLRALRRGPG/PG
US-10-475-075-243

  Query Match             1.4%;  Score 7;  DB 6;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AVLLLLL 20
              |||||||
Db          2 AVLLLLL 8


RESULT 26
US-10-475-075-513
; Sequence 513, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
;  APPLICANT: Bejanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  APPLICANT:  Dumas Milne Edwards, Jean-Baptiste
;  APPLICANT:  Jobert, Severin
;  APPLICANT:  Giordano, Jean-Yves
;  TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
;  FILE REFERENCE: G-081US03PCT
;  CURRENT APPLICATION NUMBER: US/10/475,075
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: PCT/IB01/00914
;  PRIOR FILING DATE: 2001-04-18
;  NUMBER OF SEQ ID NOS: 918
;  SOFTWARE: Patent.pm
; SEQ ID NO 513
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -16..-1
US-10-475-075-513

  Query Match             1.4%;  Score 7;  DB 6;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 AVLLLLL 20
              |||||||
Db          2 AVLLLLL 8


RESULT 27
US-10-644-807-297
; Sequence 297, Application US/10644807
; Publication No. US20060057582A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 83 Human Secreted Proteins
;  FILE REFERENCE: PS735
;  CURRENT APPLICATION NUMBER: US/10/644,807
;  CURRENT FILING DATE:  2003-08-21
;  PRIOR APPLICATION NUMBER: PCT/US02/05064
;  PRIOR FILING DATE: 2002-02-21
;  PRIOR APPLICATION NUMBER: 60/270,658
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 60/304,444
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 445
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 297
;   LENGTH: 133
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (34)
```

```
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (60)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (69)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (96)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-644-807-297

  Query Match             1.4%;  Score 7;  DB 6;  Length 133;
  Best Local Similarity   100.0%;  Pred. No. 42;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 VLLLLLL 21
              |||||||
Db         26 VLLLLLL 32


RESULT 28
US-11-096-568A-13303
; Sequence 13303, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 13303
;   LENGTH: 154
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(154)
;   OTHER INFORMATION: Ceres Seq. ID no. 15174286
US-11-096-568A-13303

  Query Match             1.4%;  Score 7;  DB 7;  Length 154;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         27 SSPSPPP 33
              |||||||
Db        132 SSPSPPP 138


RESULT 29
US-11-096-568A-22510
; Sequence 22510, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22510
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(160)
;   OTHER INFORMATION: Ceres Seq. ID no. 12409034
US-11-096-568A-22510

  Query Match             1.4%;  Score 7;  DB 7;  Length 160;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 VLLLLLL 21
              |||||||
Db         35 VLLLLLL 41


RESULT 30
US-10-467-657-2842
; Sequence 2842, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2842
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2842

  Query Match             1.4%;  Score 7;  DB 6;  Length 161;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 LAVLLLL 19
              |||||||
Db         95 LAVLLLL 101


Search completed: March 30, 2006, 09:16:46
Job time : 24 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 30, 2006, 09:08:07 ; Search time 40 Seconds
(without alignments)
1221.953 Million cell updates/sec

Title: US-10-849-979-139
Perfect score: 508
Sequence: 1 MDPKLGRMAASLLAVLLLLL.....NYIEGTKLFAAFFLEMAQLH 508

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 3510

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	10	2.0	379	2	AB1108	succinyldiaminopim
2	10	2.0	481	2	S56299	hypothetical prote
3	9	1.8	177	2	D83727	RNA polymerase ECF
4	9	1.8	248	2	E81096	CDPdiacylglycerol-
5	9	1.8	369	2	C69256	succinyl-diaminopi
6	9	1.8	400	2	B72650	hypothetical prote
7	9	1.8	473	2	T24197	hypothetical prote
8	9	1.8	497	2	S43745	phosphatidylinosit
9	9	1.8	841	2	S74280	hypothetical prote
10	8	1.6	82	2	JC7897	defensin 1 precurs
11	8	1.6	154	2	A05187	hypothetical prote
12	8	1.6	267	1	UJCH	major prion protei
13	8	1.6	267	2	A37372	prion protein homo
14	8	1.6	273	2	A46280	prion protein - ch
15	8	1.6	317	2	AF0792	conserved hypothet
16	8	1.6	325	2	T05166	quinone reductase
17	8	1.6	336	2	T45730	peroxidase-like pr
18	8	1.6	364	1	SAVLD	large surface anti
19	8	1.6	365	1	SAVLWE	large surface anti
20	8	1.6	372	2	T42426	conserved hypothet
21	8	1.6	377	2	B82846	succinyl-diaminopi
22	8	1.6	378	2	S00842	leukosialin precur
23	8	1.6	412	2	F87460	hypothetical prote
24	8	1.6	423	2	B83106	hypothetical prote
25	8	1.6	451	2	S78104	lipoprotein - Stre
26	8	1.6	463	2	D75262	C4-dicarboxylate t
27	8	1.6	522	2	T18657	hypothetical prote
28	8	1.6	545	2	F83280	probable chemotaxi
29	8	1.6	570	2	A48836	fibropellin C prec
30	8	1.6	645	2	T19382	hypothetical prote
31	8	1.6	837	2	AB3383	hypothetical membr
32	8	1.6	880	2	D89756	protein T23E7.2b [
33	8	1.6	931	2	H96527	protein F27J15.16
34	8	1.6	1002	1	GNLJND	HIV-1 retropepsin
35	7	1.4	86	2	A35241	IgE Fc receptor ga
36	7	1.4	87	2	C97909	hypothetical prote
37	7	1.4	91	2	G91275	hypothetical prote
38	7	1.4	91	2	G86116	hypothetical prote
39	7	1.4	91	2	S56424	hypothetical 10.1K
40	7	1.4	97	2	C70828	hypothetical prote
41	7	1.4	99	2	S09522	nodC protein - Rhi
42	7	1.4	107	2	T35523	probable small sec
43	7	1.4	133	2	S57038	probable membrane
44	7	1.4	135	2	AH3610	hypothetical membr
45	7	1.4	135	2	AG2045	hypothetical prote
46	7	1.4	147	2	A53180	ribonuclease PL3 (
47	7	1.4	152	2	D75367	hypothetical prote
48	7	1.4	156	2	B83138	hypothetical prote
49	7	1.4	159	2	B84669	hypothetical prote
50	7	1.4	161	2	D81940	probable membrane
51	7	1.4	161	2	E81166	hypothetical prote
52	7	1.4	168	2	B83975	hypothetical prote
53	7	1.4	169	2	B48458	surface antigen -
54	7	1.4	171	2	S19502	hypothetical prote
55	7	1.4	172	2	A49652	caltractin - human
56	7	1.4	172	2	I38424	centrin - human
57	7	1.4	172	2	S38531	caltractin - mouse
58	7	1.4	172	2	A39458	carotene biosynthe
59	7	1.4	174	2	S30200	ribosomal protein
60	7	1.4	179	2	S01400	H+-transporting tw
61	7	1.4	179	2	AH2528	hypothetical prote
62	7	1.4	182	2	AE1957	ribosome recycling
63	7	1.4	185	2	A49957	CD45-associated 30
64	7	1.4	190	2	F72207	riboflavin synthas
65	7	1.4	194	2	A72727	probable ribosomal
66	7	1.4	194	2	E82492	conserved hypothet
67	7	1.4	197	2	S51372	membrane protein L
68	7	1.4	199	2	T45543	hypothetical prote
69	7	1.4	200	2	T52627	splicing factor RS
70	7	1.4	200	2	T05112	splicing factor 9G
71	7	1.4	204	2	D75154	hypothetical prote
72	7	1.4	205	2	T48294	pathogenesis relat
73	7	1.4	206	2	A55412	lymphocyte phospha
74	7	1.4	209	1	A26166	Ig lambda-5 chain
75	7	1.4	209	2	S61856	hrpH protein - Pse
76	7	1.4	212	2	AE3591	diguanylate cyclas
77	7	1.4	221	2	F87428	conserved hypothet
78	7	1.4	221	2	JC4761	recombination acti
79	7	1.4	223	2	B95367	probable protein-L
80	7	1.4	227	2	T11825	H+-transporting tw
81	7	1.4	231	1	S74852	orotidine 5' monop
82	7	1.4	231	2	AG0785	pseudouridylate sy
83	7	1.4	231	2	F64987	hypothetical 25.9
84	7	1.4	231	2	E85857	16S pseudouridylat
85	7	1.4	231	2	C91013	16S pseudouridylat
86	7	1.4	234	2	A81871	probable periplasm
87	7	1.4	241	2	C81028	conserved hypothet
88	7	1.4	241	2	AF3327	transcription regu
89	7	1.4	247	1	A54662	myelin P0 protein
90	7	1.4	248	1	JH0252	myelin P0 protein
91	7	1.4	248	1	MPRT0	myelin P0 protein
92	7	1.4	251	2	I38053	myelin protein zer
93	7	1.4	253	2	A97052	probable lytic mur
94	7	1.4	261	2	AD2747	hypothetical prote
95	7	1.4	261	2	C97528	antigenic protein
96	7	1.4	263	2	S57346	interleukin 15 rec
97	7	1.4	271	2	A48826	low choriolytic ha
98	7	1.4	271	2	S38046	hypothetical prote
99	7	1.4	272	1	S28795	carbonate dehydrat
100	7	1.4	272	2	B83610	sulfate transport
101	7	1.4	272	2	F87269	hypothetical prote
102	7	1.4	274	2	A71140	hypothetical prote

103	7	1.4	275	2	A32410	tryptase (EC 3.4.2
104	7	1.4	284	2	S58650	hypothetical prote
105	7	1.4	287	1	S75686	suppressor protein
106	7	1.4	292	2	D71181	hypothetical prote
107	7	1.4	294	2	T34048	hypothetical prote
108	7	1.4	295	2	AI2981	ABC transporter, m
109	7	1.4	295	2	G98301	hypothetical ABC t
110	7	1.4	295	2	AE1663	transcription acti
111	7	1.4	296	2	G72760	hypothetical prote
112	7	1.4	301	2	S51439	hypothetical prote
113	7	1.4	305	2	E96622	hypothetical prote
114	7	1.4	308	2	AE2960	hypothetical prote
115	7	1.4	319	2	A98323	ABC transporter, p
116	7	1.4	319	2	S62196	hypothetical prote
117	7	1.4	323	2	T05478	peroxidase (EC 1.1
118	7	1.4	331	2	A85430	peroxidase like pr
119	7	1.4	336	2	H84767	probable peroxidas
120	7	1.4	339	2	T37487	hypothetical prote
121	7	1.4	342	2	A90894	probable transport
122	7	1.4	342	2	H85723	probable transport
123	7	1.4	351	2	S20078	NOV protein - chic
124	7	1.4	355	2	D71429	hypothetical prote
125	7	1.4	356	2	S39605	class I histocompa
126	7	1.4	359	2	PQ0468	threonine ammonia-
127	7	1.4	365	2	S66466	cathepsin E (EC 3.
128	7	1.4	365	2	B42832	factor VIII intron
129	7	1.4	366	1	SAVLBD	large surface anti
130	7	1.4	366	1	SAVLWD	large surface anti
131	7	1.4	368	2	A41111	flagellum-associat
132	7	1.4	377	2	F97267	uncharacterized co
133	7	1.4	378	2	S14959	proline-rich prote
134	7	1.4	378	2	AB1469	succinyldiaminopim
135	7	1.4	380	2	A42832	factor VIII-associ
136	7	1.4	381	2	S48049	cholecystokinin B
137	7	1.4	383	2	T21453	hypothetical prote
138	7	1.4	386	2	C81256	probable 2,3,4,5-t
139	7	1.4	389	2	G70810	probable transcrip
140	7	1.4	396	2	B64306	hypothetical prote
141	7	1.4	397	2	T00098	hypothetical prote
142	7	1.4	398	2	S66465	cathepsin E (EC 3.
143	7	1.4	398	2	C90349	multidrug-efflux t
144	7	1.4	401	2	F69834	multidrug-efflux t
145	7	1.4	405	2	A60534	P2B/LAMP-1 precurs
146	7	1.4	407	2	E89991	hypothetical prote
147	7	1.4	410	2	JC7584	basic helix-loop-h
148	7	1.4	415	2	G85066	hypothetical prote
149	7	1.4	420	2	I51667	thrombin receptor
150	7	1.4	429	2	AD2939	hypothetical prote

ALIGNMENTS

RESULT 1
AB1108
succinyldiaminopimelate desuccinylase homolog lmo0265 [imported] - Listeria monocytogene
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C;Accession: AB1108
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <GLA>
A;Cross-references: UNIPROT:Q9ZEY0; UNIPARC:UPI0000054F38; GB:NC_003210; PIDN:CAD00792.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0265
C;Superfamily: Succinyl-diaminopimelate desuccinylase

  Query Match 2.0%; Score 10; DB 2; Length 379;
  Best Local Similarity 100.0%; Pred. No. 0.21;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 GKLYGRGATD 166
||||||||||
Db 94 GKLYGRGATD 103

RESULT 2
S56299
hypothetical protein YFR044c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein F006
C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 05-Oct-2004
C;Accession: S56299; S62255; S63791
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanun
submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces cer
A;Reference number: S56186
A;Accession: S56299
A;Molecule type: DNA
A;Residues: 1-481 <MUR>
A;Cross-references: UNIPROT:P43616; UNIPARC:UPI0000052F2D; EMBL:D50617; NID:g836685; PIDN
R;Murakami, Y.
submitted to the EMBL Data Library, December 1994
A;Reference number: S62230
A;Accession: S62255
A;Molecule type: DNA
A;Residues: 1-481 <MUW>
A;Cross-references: UNIPARC:UPI0000052F2D; EMBL:D44597; NID:g871938; PIDN:BAA08010.1; PII
R;Eki, T.; Naitou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Tsuchiya, Y
Yeast 12, 149-167, 1996
A;Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI
A;Reference number: S63787; MUID:96287652; PMID:8686379
A;Accession: S63791
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-481 <EKI>
A;Cross-references: UNIPARC:UPI0000052F2D; EMBL:D44597; NID:g871938; PIDN:BAA08010.1; PII
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C;Genetics:
A;Cross-references: SGD:S0001940
A;Map position: 6R
A;Note: YFR044c
C;Superfamily: Peptidase V

  Query Match 2.0%; Score 10; DB 2; Length 481;
  Best Local Similarity 100.0%; Pred. No. 0.26;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 WRYPSLSIHG 352
||||||||||
Db 314 WRYPSLSIHG 323

RESULT 3
D83727
RNA polymerase ECF-type sigma factor sigV [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83727
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and g
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83727
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-177 <STO>
A;Cross-references: UNIPROT:Q9KF66; UNIPARC:UPI00000C392E; GB:AP001509; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: sigV

Query Match 1.8%; Score 9; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 EELVEKEKD 216
|||||||||
Db 17 EELVEKEKD 25

RESULT 4
E81096
CDPdiacylglycerol-serine O-phosphatidyltransferase (EC 2.7.8.8) NMA1532 [imported] - Nei
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: E81096; G81844
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: E81096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <TET>
A;Cross-references: UNIPROT:Q9JR61; UNIPARC:UPI00000C4E16; GB:AE002480; GB:AE002098; NID
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81844
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <PAR>
A;Cross-references: UNIPARC:UPI00000C4E16; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: pss; NMB1318; NMA1532
C;Superfamily: CDP-diacylglycerol--serine O-phosphatidyltransferase; Bacillus subtilis C
C;Keywords: transferase
F;42-192/Domain: Bacillus subtilis CDPdiacylglycerol-serine O-phosphatidyltransferase ho

Query Match 1.8%; Score 9; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLAVLLLLL 20
|||||||||
Db 204 LLAVLLLLL 212

RESULT 5
C69256
succinyl-diaminopimelate desuccinylase (dapE-1) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C;Accession: C69256
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69256
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-369 <KLE>
A;Cross-references: UNIPROT:O30185; UNIPARC:UPI0000057267; GB:AE001103; GB:AE000782; NID
C;Superfamily: Succinyl-diaminopimelate desuccinylase

Query Match 1.8%; Score 9; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 VDGKLYGRG 163
|||||||||
Db 82 VDGKLYGRG 90

RESULT 6
B72650
hypothetical protein APE0632 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C;Accession: B72650
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72650
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <KAW>
A;Cross-references: UNIPROT:Q9YEE4; UNIPARC:UPI000005DC0F; DDBJ:AP000060; NID:g5104188; P
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0632
C;Superfamily: Succinyl-diaminopimelate desuccinylase

Query Match 1.8%; Score 9; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 156 DGKLYGRGA 164
|||||||||
Db 98 DGKLYGRGA 106

RESULT 7
T24197
hypothetical protein R11H6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C;Accession: T24197
R;Bardill, S.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19852
A;Accession: T24197
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-473 <WIL>
A;Cross-references: UNIPROT:O18000; UNIPARC:UPI0000080893; EMBL:Z93386; PIDN:CAB07646.1;
A;Experimental source: clone R11H6
C;Genetics:
A;Gene: CESP:R11H6.1
A;Map position: 5
A;Introns: 101/1; 261/1
C;Superfamily: Peptidase V

Query Match 1.8%; Score 9; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 131 YGHLDVQPA 139

```
              |||||||||
Db          97 YGHLDVQPA 105


RESULT 8
S43745
phosphatidylinositol-phosphatidylcholine transfer protein SEC14 - yeast (Yarrowia lipoly
C;Species: Yarrowia lipolytica, Candida lipolytica
C;Date: 03-May-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S43745
R;Lopez, M.; Nicaud, J.; Vergnolle, C.; Kader, J.; Bankaitis, V.; Gaillardin, C.
submitted to the EMBL Data Library, July 1993
A;Description: A phospholipid transfer protein is required for dimorphic transition in t
A;Reference number: S43745
A;Accession: S43745
A;Molecule type: DNA
A;Residues: 1-497 <LOP>
A;Cross-references: UNIPROT:P45816; UNIPARC:UPI00001355BB; EMBL:L20972; NID:g311166; PID
C;Genetics:
A;Gene: SEC14
A;Introns: 6/3; 9/2
F;58-265/Domain: cellular retinaldehyde-binding protein homology <CRB>

  Query Match             1.8%;  Score 9;  DB 2;  Length 497;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 LLAVLLLLL 20
               |||||||||
Db         349 LLAVLLLLL 357


RESULT 9
S74280
hypothetical protein YCL054w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YCL431
C;Species: Saccharomyces cerevisiae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74280; S19384; S19744; S25340
R;Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, September 1996
A;Reference number: S74277
A;Accession: S74280
A;Molecule type: DNA
A;Residues: 1-841 <VOE>
A;Cross-references: UNIPROT:P25582; UNIPARC:UPI0000053220; EMBL:X59720; NID:g1907116; PI
R;Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19384
A;Accession: S19384
A;Molecule type: DNA
A;Residues: 1-213 <VOW>
A;Cross-references: UNIPARC:UPI000017CCFB; EMBL:X59720; MIPS:YCL054w
A;Note: this sequence has been revised in reference S74280
R;Fuller, L.J.; Kelly, A.; Lewis, C.; McKee, R.A.; Pearson, B.M.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19380
A;Accession: S19744
A;Molecule type: DNA
A;Residues: 213-724 <FUL>
A;Cross-references: UNIPARC:UPI000017CCFC; EMBL:X59720; MIPS:YCL054w
R;Defoor, E.; Debrabandere, R.; Keyers, B.; Voet, M.; Volckaert, G.
Yeast 8, 681-687, 1992
A;Title: Nucleotide sequence of D10B, a BamHI fragment on the small-ring chromosome III
A;Reference number: S25338; MUID:93070606; PMID:1441748
A;Accession: S25340
A;Molecule type: DNA
A;Residues: 1-214 <DEF>
A;Cross-references: UNIPARC:UPI000017CCFD; EMBL:X59720
C;Genetics:
A;Gene: SGD:SPB1
A;Cross-references: SGD:S0000559
A;Map position: 3L
A;Note: YCL054w

  Query Match             1.8%;  Score 9;  DB 2;  Length 841;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         299 EVVPLTEEE 307
               |||||||||
Db         342 EVVPLTEEE 350


RESULT 10
JC7897
defensin 1 precursor - wheat
C;Species: Triticum aestivum (common wheat)
C;Date: 03-Feb-2003 #sequence_revision 03-Feb-2003 #text_change 09-Jul-2004
C;Accession: JC7897
R;Koike, M.; Okamoto, T.; Tsuda, S.; Imai, R.
Biochem. Biophys. Res. Commun. 298, 46-53, 2002
A;Title: A novel plant defensin-like gene of winter wheat is specifically induced during
A;Reference number: JC7897; MUID:22266815; PMID:12379218
A;Accession: JC7897
A;Molecule type: mRNA
A;Residues: 1-82 <KOI>
A;Cross-references: UNIPROT:Q8L698; UNIPARC:UPI00000A3AB3; DDBJ:AB089942
A;Experimental source: crown tissue
C;Comment: This protein is an antipathogenic protein and belongs to a subfamily of thioni
d tolerance against pathogens during cold acclimation.
C;Genetics:
A;Gene: Tad1

  Query Match             1.6%;  Score 8;  DB 2;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 5.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          14 AVLLLLLL 21
               ||||||||
Db          12 AVLLLLLL 19


RESULT 11
A05187
hypothetical protein 154 - common tobacco chloroplast
C;Species: chloroplast Nicotiana tabacum (common tobacco)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Sep-1999
C;Accession: A05187
R;Sugiura, M.
submitted to the EMBL Data Library, August 1986
A;Reference number: A00149
A;Accession: A05187
A;Molecule type: DNA
A;Residues: 1-154 <SUG>
A;Cross-references: UNIPARC:UPI00001791FD
A;Experimental source: cv. Bright Yellow 4
R;Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Matsubayashi, T.; Zai
Deno, H.; Kamogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Tohdoh, N.; Shi
EMBO J. 5, 2043-2049, 1986
A;Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene org
A;Reference number: A38013
A;Contents: annotation; gene organization, sites, features
C;Genetics:
A;Genome: chloroplast
C;Superfamily: common tobacco chloroplast hypothetical protein 154
C;Keywords: chloroplast

  Query Match             1.6%;  Score 8;  DB 2;  Length 154;
  Best Local Similarity   100.0%;  Pred. No. 8.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          18 LLLLERGM 25
               ||||||||
Db         100 LLLLERGM 107
```

RESULT 12
UJCH
major prion protein homolog precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A41280; B41280
R;Harris, D.A.; Falls, D.L.; Johnson, F.A.; Fischbach, G.D.
Proc. Natl. Acad. Sci. U.S.A. 88, 7664-7668, 1991
A;Title: A prion-like protein from chicken brain copurifies with an acetylcholine recept
A;Reference number: A41280; MUID:91352049; PMID:1715573
A;Accession: A41280
A;Molecule type: mRNA
A;Residues: 1-267 <HAR>
A;Cross-references: UNIPROT:P27177; UNIPARC:UPI0000171396; GB:M61145; NID:g212614; PIDN:
A;Experimental source: day-18 brain
A;Accession: B41280
A;Molecule type: protein
A;Residues: 25-51 <HA2>
A;Cross-references: UNIPARC:UPI0000174093
A;Note: the protein was purified from adult chicken brain on the basis of its ability to
C;Comment: Enzymatic release studies show that this protein has a glycosylphosphatidylin
C;Superfamily: major prion protein
C;Keywords: brain; glycoprotein; phosphatidylinositol linkage; prion; scrapie
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-267/Product: major prion protein homolog #status predicted <MAT>
F;188,203,212/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 1.6%; Score 8; DB 1; Length 267;
  Best Local Similarity 100.0%; Pred. No. 14;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAVLLLL 20
 ||||||||
Db 253 LAVLLLL 260

RESULT 13
A37372
prion protein homolog precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 07-May-1999
C;Accession: A37372
R;Falls, D.L.; Harris, D.A.; Johnson, F.A.; Morgan, M.M.; Corfas, G.; Fischbach, G.D.
Cold Spring Harb. Symp. Quant. Biol. 55, 397-406, 1990
A;Title: M-r 42,000 ARIA: a protein that may regulate the accumulation of acetylcholine
A;Reference number: A37372; MUID:92111159; PMID:2132829
A;Accession: A37372
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-267 <FAL>
A;Cross-references: UNIPARC:UPI00001777FA; GB:M61145
C;Superfamily: major prion protein

  Query Match 1.6%; Score 8; DB 2; Length 267;
  Best Local Similarity 100.0%; Pred. No. 14;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAVLLLL 20
 ||||||||
Db 253 LAVLLLL 260

RESULT 14
A46280
prion protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46280
R;Gabriel, J.M.; Oesch, B.; Kretzschmar, H.; Scott, M.; Prusiner, S.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 9097-9101, 1992
A;Title: Molecular cloning of a candidate chicken prion protein.
A;Reference number: A46280; MUID:93028411; PMID:1409608
A;Accession: A46280
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-273 <GAB>
A;Cross-references: UNIPROT:P27177; UNIPARC:UPI0000132205; GB:M95404; NID:g212610; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:115392, NCBIP:115393)
C;Superfamily: major prion protein

  Query Match 1.6%; Score 8; DB 2; Length 273;
  Best Local Similarity 100.0%; Pred. No. 15;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAVLLLL 20
 ||||||||
Db 259 LAVLLLL 266

RESULT 15
AF0792
conserved hypothetical protein STY2517 [imported] - Salmonella enterica subsp. enterica s
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0792
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0792
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-317 <PAR>
A;Cross-references: UNIPARC:UPI00000CDB87; GB:AL513382; PIDN:CAD07520.1; PID:g16503513; C
C;Genetics:
A;Gene: STY2517

  Query Match 1.6%; Score 8; DB 2; Length 317;
  Best Local Similarity 100.0%; Pred. No. 17;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 326 RVEKFLFD 333
 ||||||||
Db 37 RVEKFLFD 44

RESULT 16
T05166
quinone reductase homolog F18E5.200 - Arabidopsis thaliana
N;Alternate names: hypothetical protein F17L22.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05166; T05833
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mewe
submitted to the Protein Sequence Database, August 1998
A;Reference number: Z15400
A;Accession: T05166
A;Molecule type: DNA
A;Residues: 1-325 <BEV>
A;Cross-references: UNIPROT:O65423; UNIPARC:UPI000009F5A5; EMBL:ALO22603
A;Experimental source: cultivar Columbia; BAC clone F18E5
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Bar
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15454
A;Accession: T05833
A;Molecule type: DNA
A;Residues: 1-325 <BEW>
A;Cross-references: UNIPARC:UPI000009F5A5; EMBL:AL035527
A;Experimental source: cultivar Columbia; BAC clone F17L22
C;Genetics:
A;Map position: 4

A;Introns: 84/3; 144/3; 172/1; 261/1
A;Note: F18B5.200; F17L22.40
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 1.6%; Score 8; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 83 ADTLQRLG 90
||||||||
Db 42 ADTLQRLG 49

RESULT 17
T45730
peroxidase-like protein - Arabidopsis thaliana
N;Alternate names: protein F24M12.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45730
R;Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23012
A;Accession: T45730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <VIT>
A;Cross-references: UNIPROT:Q9SD46; UNIPARC:UPI000004882D; EMBL:AL132980
A;Experimental source: cultivar Columbia; BAC clone F24M12
C;Genetics:
A;Map position: 3
A;Introns: 78/3; 142/3; 198/1
A;Note: F24M12.30
C;Superfamily: peroxidase

Query Match 1.6%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 276 DLVALLGS 283
||||||||
Db 192 DLVALLGS 199

RESULT 18
SAVLD
large surface antigen - duck hepatitis virus
N;Contains: major surface antigen; middle surface antigen
C;Species: duck hepatitis virus, DHBV
C;Date: 20-Sep-1984 #sequence_revision 20-Sep-1984 #text_change 31-Dec-2004
C;Accession: A03710; S12845
R;Mandart, E.; Kay, A.; Galibert, F.
J. Virol. 49, 782-792, 1984
A;Title: Nucleotide sequence of a cloned duck hepatitis B virus genome: comparison with
A;Reference number: A92997; MUID:84138772; PMID:6699938
A;Accession: A03710
A;Molecule type: DNA
A;Residues: 1-364 <MAN>
A;Cross-references: UNIPROT:O92935; UNIPARC:UPI0000174975; GB:K01834
R;Mattes, F.; Tong, S.; Teubner, K.; Blum, H.E.
Nucleic Acids Res. 18, 6140, 1990
A;Title: Complete nucleotide sequence of a German duck hepatitis B virus.
A;Reference number: S12843; MUID:91045092; PMID:2235507
A;Accession: S12845
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 36-364 <MAT>
A;Cross-references: UNIPARC:UPI00000F9AFA; EMBL:X12798
C;Genetics:
A;Gene: pre-S1/pre-S2/S
C;Keywords: glycoprotein; surface antigen
F;89-364/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F;198-364/Product: major surface antigen (gene S) #status predicted <MSA>
F;32,170,296/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.6%; Score 8; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 SGTFGGIL 270
||||||||
Db 199 SGTFGGIL 206

RESULT 19
SAVLWE
large surface antigen - duck hepatitis virus (strain China)
N;Contains: major surface antigen; middle surface antigen
C;Species: duck hepatitis virus, DHBV
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S12842
R;Tong, S.; Mattes, F.; Teubner, K.; Blum, H.E.
Nucleic Acids Res. 18, 6139, 1990
A;Title: Complete nucleotide sequence of a Chinese duck hepatitis B virus.
A;Reference number: S12840; MUID:91045091; PMID:2235506
A;Accession: S12842
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-365 <TON>
A;Cross-references: UNIPROT:P30029; UNIPARC:UPI00001389B2; GB:M21953; NID:g325435; PIDN:
C;Genetics:
A;Gene: pre-S1/pre-S2/S
C;Superfamily: hepatitis B virus surface antigen
C;Keywords: glycoprotein; surface antigen
F;89-365/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F;199-365/Product: major surface antigen (gene S) #status predicted <MSA>
F;297/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.6%; Score 8; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 263 SGTFGGIL 270
||||||||
Db 200 SGTFGGIL 207

RESULT 20
T42426
conserved hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Accession: T42426
R;Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A;Reference number: Z17323; MUID:98162722; PMID:9501991
A;Accession: T42426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-372 <YOS>
A;Cross-references: UNIPROT:P78801; UNIPARC:UPI000006C66C; EMBL:D89150; NID:g1749507; PII
A;Experimental source: strain PR745
C;Superfamily: Peptidase V

Query Match 1.6%; Score 8; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 370 VIGKFSIR 377
||||||||
Db 268 VIGKFSIR 275

RESULT 21
B82846

succinyl-diaminopimelate desuccinylase XF0116 [imported] - Xylella fastidiosa (strain 9a
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: B82846
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82846
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <SIM>
A;Cross-references: UNIPROT:Q9PH30; UNIPARC:UPI00000C22DE; GB:AE003865; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0116
C;Superfamily: Succinyl-diaminopimelate desuccinylase

  Query Match 1.6%; Score 8; DB 2; Length 377;
  Best Local Similarity 100.0%; Pred. No. 19;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 157 GKLYGRGA 164
 ||||||||
Db 90 GKLYGRGA 97

RESULT 22
S00842
leukosialin precursor - rat (fragment)
N;Alternate names: leucocyte sialoglycoprotein; sialophorin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S00842
R;Killeen, N.; Barclay, A.N.; Willis, A.C.; Williams, A.F.
EMBO J. 6, 4029-4034, 1987
A;Title: The sequence of rat leukosialin (W3/13 antigen) reveals a molecule with O-linke
A;Reference number: S00842; MUID:88166646; PMID:2965006
A;Accession: S00842
A;Molecule type: mRNA
A;Residues: 1-378 <KIL>
A;Cross-references: UNIPROT:P13838; UNIPARC:UPI000012E5AB; EMBL:Y00090; NID:g56573; PIDN
C;Superfamily: leukosialin
C;Keywords: glycoprotein; transmembrane protein
F;1-7/Domain: signal sequence #status predicted <SIG>
F;8-378/Product: leukosialin #status predicted <MAT>

  Query Match 1.6%; Score 8; DB 2; Length 378;
  Best Local Similarity 100.0%; Pred. No. 19;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 203 GSVALEEL 210
 ||||||||
Db 329 GSVALEEL 336

RESULT 23
F87460
hypothetical protein CC1706 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87460
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-412 <STO>
A;Cross-references: UNIPROT:Q9A7L6; UNIPARC:UPI00000C7493; GB:AE005673; NID:g13423120; PI
C;Genetics:
A;Gene: CC1706

  Query Match 1.6%; Score 8; DB 2; Length 412;
  Best Local Similarity 100.0%; Pred. No. 21;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 AVLLLLLL 21
 ||||||||
Db 6 AVLLLLLL 13

RESULT 24
B83106
hypothetical protein PA4321 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83106
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-423 <STO>
A;Cross-references: UNIPROT:Q9HW80; UNIPARC:UPI00000C5CB9; GB:AE004848; GB:AE004091; NID:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4321

  Query Match 1.6%; Score 8; DB 2; Length 423;
  Best Local Similarity 100.0%; Pred. No. 22;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLAVLLLL 19
 ||||||||
Db 10 LLAVLLLL 17

RESULT 25
S78104
lipoprotein - Streptomyces antibioticus
C;Species: Streptomyces antibioticus
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S78104; S33183
R;Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.
submitted to the EMBL Data Library, September 1993
A;Description: Characterization of a Streptomyces antibioticus gene cluster encoding a gl
A;Reference number: S78104
A;Accession: S78104
A;Molecule type: DNA
A;Residues: 1-451 <HER>
A;Cross-references: UNIPROT:Q53684; UNIPARC:UPI000013BC70; EMBL:Z22577; NID:g404284; PIDN
A;Experimental source: strain ATCC 11891
A;Note: this is a revision to the sequence from reference S33182

R;Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.
submitted to the EMBL Data Library, April 1993
A;Description: Characterization of a Streptomyces antibioticus gene cluster encoding a g
A;Reference number: S33182
A;Accession: S33183
A;Molecule type: DNA
A;Residues: 1-422,'LPALTR',429-430,'AY',433,'AQE',437,'EIYE',444,'Q',446-447,'VYRRRRDHPD
A;Cross-references: UNIPARC:UPI000017AD90; EMBL:Z22577
A;Experimental source: strain ATCC 11891
A;Note: this sequence has been revised in reference S78104

Query Match 1.6%; Score 8; DB 2; Length 451;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LAVLLLLL 20
||||||||
Db 9 LAVLLLLL 16

RESULT 26
D75262
C4-dicarboxylate transport protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75262
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75262
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-463 <WHI>
A;Cross-references: UNIPARC:UPI0000164CCF; GB:AE002082; GB:AE000513; NID:g6460347; PIDN:
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2525
A;Map position: 1
C;Superfamily: C4-dicarboxylate carrier protein

Query Match 1.6%; Score 8; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 SLLAVLLL 18
||||||||
Db 350 SLLAVLLL 357

RESULT 27
T18657
hypothetical protein B0035.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18657
R;White, S.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19002
A;Accession: T18657
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-522 <WIL>
A;Cross-references: UNIPROT:Q27464; UNIPARC:UPI000012AF14; EMBL:Z73102; PIDN:CAA97412.1;
A;Experimental source: clone B0035
C;Genetics:
A;Gene: CESP:B0035.5
A;Map position: 4
A;Introns: 42/3; 111/3; 137/1; 221/2; 322/1; 368/1; 435/2; 494/2
C;Superfamily: glucose-6-phosphate dehydrogenase

Query Match 1.6%; Score 8; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 188 LPVNIKFI 195
||||||||
Db 63 LPVNIKFI 70

RESULT 28
F83280
probable chemotaxis transducer PA2920 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83280
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83280
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-545 <STO>
A;Cross-references: UNIPROT:Q9HZS7; UNIPARC:UPI00000C5883; GB:AE004718; GB:AE004091; NID:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2920

Query Match 1.6%; Score 8; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LLAVLLLL 19
||||||||
Db 20 LLAVLLLL 27

RESULT 29
A48836
fibropellin C precursor - sea urchin (Strongylocentrotus purpuratus)
N;Alternate names: EGF repeat-containing protein; epidermal growth factor-related protein
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48836
R;Bisgrove, B.W.; Raff, R.A.
Dev. Biol. 157, 526-538, 1993
A;Title: The SpEGF III gene encodes a member of the fibropellins: EGF repeat-containing p
A;Reference number: A48836; MUID:93273088; PMID:8500658
A;Accession: A48836
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-570 <BIS>
A;Cross-references: UNIPROT:P49013; UNIPARC:UPI000012A573; GB:L07045; NID:g310659; PID:g3
A;Note: sequence extracted from NCBI backbone (NCBIN:132724, NCBIP:132725)
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-570/Product: fibropellin C #status predicted <FIB>
F;19-54/Domain: EGF homology <EG1>
F;57-175/Domain: C1r/C1s repeat homology <C1R>
F;176-211/Domain: EGF homology <EG2>
F;214-249/Domain: EGF homology <EG3>
F;252-287/Domain: EGF homology <EG4>
F;290-325/Domain: EGF homology <EG5>
F;328-363/Domain: EGF homology <EG6>
F;366-401/Domain: EGF homology <EG7>
F;404-439/Domain: EGF homology <EG8>
F;442-570/Region: avidin-like
F;23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27
fide bonds: #status predicted

Query Match 1.6%; Score 8; DB 2; Length 570;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         11 SLLAVLLL 18
              ||||||||
Db          4 SLLAVLLL 11
```

RESULT 30
T19382
hypothetical protein C18D1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19382
R;Berks, M.
submitted to the EMBL Data Library, March 1995
A;Reference number: Z19117
A;Accession: T19382
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-645 <WIL>
A;Cross-references: UNIPROT:Q09478; UNIPARC:UPI000008359C; EMBL:Z48543; PIDN:CAA88432.1;
A;Experimental source: clone C18D1
C;Genetics:
A;Gene: CESP:C18D1.1
A;Map position: 2
A;Introns: 16/3; 133/3; 296/3; 574/3; 611/1

Query Match 1.6%; Score 8; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         27 SSPSPPPA 34
              ||||||||
Db        144 SSPSPPPA 151
```

Search completed: March 30, 2006, 09:12:35
Job time : 45 secs

OM protein - protein search, using sw model

Run on: March 30, 2006, 09:04:47 ; Search time 233 Seconds
(without alignments)
1538.233 Million cell updates/sec

Title: US-10-849-979-139
Perfect score: 508
Sequence: 1 MDPKLGRMAASLLAVLLLLL.....NYIEGTKLFAAFFLEMAQLH 508

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 6

Total number of hits satisfying chosen parameters: 34363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 150 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	407	80.1	508	1	CPGL2_HUMAN	Q96kn2 homo sapien
2	148	29.1	171	2	Q6ZND4_HUMAN	Q6znd4 homo sapien
3	145	28.5	464	2	Q5RA69_PONPY	Q5ra69 pongo pygma
4	32	6.3	492	2	Q80XP5_MOUSE	Q80xp5 mus musculu
5	32	6.3	492	2	Q8BUG2_MOUSE	Q8bug2 mus musculu
6	30	5.9	492	2	Q66HG3_RAT	Q66hg3 rattus norv
7	15	3.0	357	2	Q8I1B0_DROWI	Q8i1b0 drosophila
8	15	3.0	471	2	Q8I1J9_DROVI	Q8i1j9 drosophila
9	15	3.0	478	2	Q6C1A8_YARLI	Q6c1a8 yarrowia li
10	15	3.0	478	2	Q4WWD5_ASPFU	Q4wwd5 aspergillus
11	15	3.0	489	2	Q8AWF8_XENLA	Q8awf8 xenopus lae
12	15	3.0	494	2	Q7ZXA6_XENLA	Q7zxa6 xenopus lae
13	15	3.0	500	2	Q801E4_XENLA	Q801e4 xenopus lae
14	13	2.6	494	2	Q6PA54_XENLA	Q6pa54 xenopus lae
15	11	2.2	184	2	Q7ZZU2_OREMO	Q7zzu2 oreochromis
16	11	2.2	407	2	Q4RLC4_TETNG	Q4rlc4 tetraodon n
17	11	2.2	474	2	Q6DH98_BRARE	Q6dh98 brachydanio
18	11	2.2	474	2	Q6DJK5_XENLA	Q6djk5 xenopus lae
19	11	2.2	474	2	Q6P358_XENTR	Q6p358 xenopus tro
20	11	2.2	474	2	Q6TNV3_BRARE	Q6tnv3 brachydanio
21	11	2.2	474	2	Q7T0R7_XENLA	Q7t0r7 xenopus lae
22	11	2.2	475	2	Q5ZLV5_CHICK	Q5zlv5 gallus gall
23	11	2.2	477	2	Q5B7M1_EMENI	Q5b7m1 aspergillus
24	11	2.2	478	2	Q9V9H1_DROME	Q9v9h1 drosophila
25	10	2.0	26	2	Q9ESQ6_MOUSE	Q9esq6 mus musculu
26	10	2.0	156	2	Q6QMP8_LISMO	Q6qmp8 listeria mo
27	10	2.0	157	2	Q6QMP6_LISMO	Q6qmp6 listeria mo
28	10	2.0	157	2	Q6QMQ0_LISMO	Q6qmq0 listeria mo
29	10	2.0	159	2	Q83UJ0_LISMO	Q83uj0 listeria mo
30	10	2.0	159	2	Q84GK9_LISMO	Q84gk9 listeria mo
31	10	2.0	351	2	Q8TZ13_METKA	Q8tz13 methanopyru
32	10	2.0	379	2	Q9EXF4_LISMO	Q9exf4 listeria mo
33	10	2.0	379	2	Q9ZEY0_LISMO	Q9zey0 listeria mo
34	10	2.0	455	2	Q4SUU3_TETNG	Q4suu3 tetraodon n
35	10	2.0	476	2	Q4HYR5_GIBZE	Q4hyr5 gibberella
36	10	2.0	481	1	CPGL_YEAST	P43616 saccharomyc
37	10	2.0	483	2	Q6FWY0_CANGA	Q6fwy0 candida gla
38	10	2.0	501	1	PTGIS_MOUSE	O35074 mus musculu
39	10	2.0	501	1	PTGIS_RAT	Q62969 rattus norv
40	10	2.0	509	2	Q8BXC0_MOUSE	Q8bxc0 mus musculu
41	10	2.0	533	2	Q6CYE6_KLULA	Q6cye6 kluyveromyc
42	10	2.0	607	2	Q5W239_MAIZE	Q5w239 zea mays (m
43	10	2.0	1030	2	Q4ITX0_AZOVI	Q4itx0 azotobacter
44	9	1.8	99	2	Q4T6H3_TETNG	Q4t6h3 tetraodon n
45	9	1.8	100	2	Q9LDG6_ORYSA	Q9ldg6 oryza sativ
46	9	1.8	103	2	Q4VXS4_HUMAN	Q4vxs4 homo sapien
47	9	1.8	170	2	Q9NUV1_HUMAN	Q9nuv1 homo sapien
48	9	1.8	173	2	Q6XHG1_DROYA	Q6xhg1 drosophila
49	9	1.8	177	2	Q9KF66_BACHD	Q9kf66 bacillus ha
50	9	1.8	194	2	Q6UX25_HUMAN	Q6ux25 homo sapien
51	9	1.8	194	2	Q4VXS6_HUMAN	Q4vxs6 homo sapien
52	9	1.8	209	2	Q8NDY8_HUMAN	Q8ndy8 homo sapien
53	9	1.8	225	2	Q84ZC8_ORYSA	Q84zc8 oryza sativ
54	9	1.8	248	2	Q5F920_NEIG1	Q5f920 neisseria g
55	9	1.8	248	2	Q9JR61_NEIMA	Q9jr61 neisseria m
56	9	1.8	248	2	Q7DDC6_NEIMB	Q7ddc6 neisseria m
57	9	1.8	252	2	Q7P3P6_FUSNV	Q7p3p6 fusobacteri
58	9	1.8	276	2	Q9H7K8_HUMAN	Q9h7k8 homo sapien
59	9	1.8	311	2	Q9NW02_HUMAN	Q9nw02 homo sapien
60	9	1.8	369	2	O30185_ARCFU	O30185 archaeoglob
61	9	1.8	378	2	Q82Z92_ENTFA	Q82z92 enterococcu
62	9	1.8	379	2	Q4LN79_9BURK	Q4ln79 burkholderi
63	9	1.8	379	2	Q62JB1_BURMA	Q62jb1 burkholderi
64	9	1.8	383	2	Q63T00_BURPS	Q63t00 burkholderi
65	9	1.8	386	2	Q8XZK5_RALSO	Q8xzk5 ralstonia s
66	9	1.8	391	2	Q8WY59_HUMAN	Q8wy59 homo sapien
67	9	1.8	400	2	Q9YEE4_AERPE	Q9yee4 aeropyrum p
68	9	1.8	401	2	Q6KAT3_MOUSE	Q6kat3 mus musculu
69	9	1.8	403	2	Q5WZP6_LEGPL	Q5wzp6 legionella
70	9	1.8	406	2	Q89T45_BRAJA	Q89t45 bradyrhizob
71	9	1.8	411	2	Q8KNB1_PSEAE	Q8knb1 pseudomonas
72	9	1.8	411	2	Q9XC62_PSEAE	Q9xc62 pseudomonas
73	9	1.8	418	2	Q67UY9_ORYSA	Q67uy9 oryza sativ
74	9	1.8	443	2	Q9BL46_CAEEL	Q9bl46 caenorhabdi
75	9	1.8	471	2	Q61JD3_CAEBR	Q61jd3 caenorhabdi
76	9	1.8	473	2	Q61W41_CAEBR	Q61w41 caenorhabdi
77	9	1.8	473	2	O18000_CAEEL	O18000 caenorhabdi
78	9	1.8	475	1	CPGL1_HUMAN	Q96kp4 homo sapien
79	9	1.8	475	1	CPGL1_MOUSE	Q9d1a2 mus musculu
80	9	1.8	475	2	Q5R432_PONPY	Q5r432 pongo pygma
81	9	1.8	475	2	Q5R5I0_PONPY	Q5r5i0 pongo pygma
82	9	1.8	475	2	Q6Q0N1_RAT	Q6q0n1 rattus norv
83	9	1.8	476	2	Q560T2_CRYNE	Q560t2 cryptococcu
84	9	1.8	476	2	Q5KPT1_CRYNE	Q5kpt1 cryptococcu
85	9	1.8	477	2	Q4PCK5_USTMA	Q4pck5 ustilago ma
86	9	1.8	477	2	Q7QJQ9_ANOGA	Q7qjq9 anopheles g
87	9	1.8	499	2	Q6P336_XENTR	Q6p336 xenopus tro
88	9	1.8	512	2	Q8RG48_FUSNN	Q8rg48 fusobacteri
89	9	1.8	519	2	Q7NIC7_GLOVI	Q7nic7 gloeobacter
90	9	1.8	790	2	Q53U95_MAIZE	Q53u95 zea mays (m
91	9	1.8	832	2	Q4I3K7_GIBZE	Q4i3k7 gibberella
92	9	1.8	841	1	SPB1_YEAST	P25582 saccharomyc
93	9	1.8	896	2	Q4NY52_9DELT	Q4ny52 anaeromyxob
94	9	1.8	908	2	Q4FVY0_LEIMA	Q4fvy0 leishmania
95	9	1.8	947	2	Q4NS17_9DELT	Q4ns17 anaeromyxob
96	8	1.6	53	2	Q6H8C6_ORYSA	Q6h8c6 oryza sativ
97	8	1.6	82	2	Q8L698_WHEAT	Q8l698 triticum ae
98	8	1.6	86	2	Q6R529_ORENI	Q6r529 oreochromis
99	8	1.6	110	2	Q53AN3_ORYSA	Q53an3 oryza sativ
100	8	1.6	111	2	Q6R528_ORENI	Q6r528 oreochromis
101	8	1.6	114	1	NPFF_RAT	Q9wva9 rattus norv
102	8	1.6	115	2	Q6UXD1_HUMAN	Q6uxd1 homo sapien
103	8	1.6	115	2	Q7U487_SYNPX	Q7u487 synechococc
104	8	1.6	115	2	Q6R530_ORENI	Q6r530 oreochromis

105	8	1.6	118	2	Q8BHM3_MOUSE	Q8bhm3 m mus muscu
106	8	1.6	138	1	LSHB_MACRU	O46483 macropus ru
107	8	1.6	146	2	Q6IID7_DROME	Q6iid7 drosophila
108	8	1.6	165	2	Q9IXF7_9HIV1	Q9ixf7 human immun
109	8	1.6	166	2	Q88JE9_PSEPK	Q88je9 pseudomonas
110	8	1.6	167	2	Q4LL26_9BURK	Q4ll26 burkholderi
111	8	1.6	167	2	Q6QJC5_HPBDU	Q6qjc5 duck hepati
112	8	1.6	167	2	Q6RSF0_HPBDU	Q6rsf0 duck hepati
113	8	1.6	167	2	Q6RSF5_HPBDU	Q6rsf5 duck hepati
114	8	1.6	167	2	Q9WFA7_9HEPA	Q9wfa7 snow goose
115	8	1.6	167	2	Q9WFB0_9HEPA	Q9wfb0 snow goose
116	8	1.6	167	2	Q9WFB4_9HEPA	Q9wfb4 snow goose
117	8	1.6	167	2	Q9WFB7_9HEPA	Q9wfb7 snow goose
118	8	1.6	167	2	Q89689_HPBDU	Q89689 duck hepati
119	8	1.6	170	1	DEF1_BORBR	Q7wqs9 bordetella
120	8	1.6	170	1	DEF1_BORPA	Q7w1v3 bordetella
121	8	1.6	170	1	DEF2_BORPE	Q7vs88 bordetella
122	8	1.6	174	2	Q76MH1_9TELE	Q76mh1 saccopharyn
123	8	1.6	180	2	Q6IK38_DROME	Q6ik38 drosophila
124	8	1.6	183	2	Q6Z1A0_ORYSA	Q6z1a0 oryza sativ
125	8	1.6	192	2	Q64FU1_HORSE	Q64fu1 equus cabal
126	8	1.6	204	2	Q75SY2_ECOLI	Q75sy2 escherichia
127	8	1.6	206	1	RL25_THET2	Q72ia7 thermus the
128	8	1.6	206	1	RL25_THET8	Q5shz1 thermus the
129	8	1.6	206	1	RL25_THETH	P56930 thermus the
130	8	1.6	208	2	Q5KVW6_GEOKA	Q5kvw6 geobacillus
131	8	1.6	209	2	Q9SS31_ARATH	Q9ss31 arabidopsis
132	8	1.6	210	2	Q75SX6_ECOLI	Q75sx6 escherichia
133	8	1.6	211	2	Q74MG5_NANEQ	Q74mg5 nanoarchaeu
134	8	1.6	234	2	Q75GL3_ORYSA	Q75gl3 oryza sativ
135	8	1.6	237	2	Q9WGS2_9HIV1	Q9wgs2 human immun
136	8	1.6	237	2	Q9WGV8_9HIV1	Q9wgv8 human immun
137	8	1.6	237	2	Q9WGW0_9HIV1	Q9wgw0 human immun
138	8	1.6	237	2	Q9WGW1_9HIV1	Q9wgw1 human immun
139	8	1.6	238	2	Q67WD8_ORYSA	Q67wd8 oryza sativ
140	8	1.6	243	2	Q7PVG9_ANOGA	Q7pvg9 anopheles g
141	8	1.6	248	2	Q8L275_PROVU	Q8l275 proteus vul
142	8	1.6	262	1	PYRK_METKA	P58887 methanopyru
143	8	1.6	270	1	UPPP1_BACC1	P62461 bacillus ce
144	8	1.6	270	1	UPPP1_BACCR	Q81hv4 bacillus ce
145	8	1.6	270	1	UPPP2_BACCZ	Q63fw2 bacillus ce
146	8	1.6	270	1	UPPP2_BACHK	Q6hnd2 bacillus th
147	8	1.6	270	1	UPPP3_BACAN	Q81v21 bacillus an
148	8	1.6	270	2	Q4ML30_BACCE	Q4ml30 bacillus ce
149	8	1.6	273	1	PRIO_CHICK	P27177 gallus gall
150	8	1.6	273	2	Q6JM13_MELUD	Q6jm13 melopsittac

ALIGNMENTS

```
RESULT 1
CPGL2_HUMAN
ID   CPGL2_HUMAN    STANDARD;      PRT;   508 AA.
AC   Q96KN2; Q6UWK2; Q9BT98;
DT   28-FEB-2003 (Rel. 41, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Glutamate carboxypeptidase-like protein 2 precursor (CNDP dipeptidase
DE   1).
GN   Name=CNDP1; Synonyms=CPGL2; ORFNames=UNQ1915/PRO4380;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Chen J.M., Barrett A.J.;
RT   "Cloning and sequencing of a second human homologue of glutamate
RT   carboxypeptidase in peptidase family M20.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 199-508.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: Belongs to the peptidase M20A family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AJ417564; CAD10388.1; -; mRNA.
DR   EMBL; AY358756; AAQ89116.1; -; mRNA.
DR   EMBL; BC004271; -; NOT_ANNOTATED_CDS; mRNA.
DR   MEROPS; M20.006; -.
DR   Ensembl; ENSG00000150656; Homo sapiens.
DR   HGNC; HGNC:20675; CNDP1.
DR   MIM; 609064; -.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00758; ARGE_DAPE_CPG2_1; FALSE_NEG.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
KW   Carboxypeptidase; Hydrolase; Metalloprotease; Protease; Signal.
FT   SIGNAL        1     27       Potential.
FT   CHAIN        28    508       Glutamate carboxypeptidase-like protein
FT                                2.
FT   CONFLICT     21     21       Missing (in Ref. 2).
FT   CONFLICT    156    156       G -> D (in Ref. 2).
FT   CONFLICT    238    238       P -> L (in Ref. 1).
FT   CONFLICT    273    273       P -> L (in Ref. 1).
SQ   SEQUENCE   508 AA;  56747 MW;  8B9EA15F4277553E CRC64;
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  Query Match           80.1%;  Score 407;  DB 1;  Length 508;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches  507;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI 60

Qy         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ESDSVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 120

Qy        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSA 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        121 SDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVGGKLYGRGATDNKGPVLAWINAVSA 180

Qy        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAI 240

Qy        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV 300

Qy        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEP 360

Qy        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWI 420

Qy        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHS 480

Qy        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508
              ||||||||||||||||||||||||||||
Db        481 QNEKINRWNYIEGTKLFAAFFLEMAQLH 508


RESULT 2
Q6ZND4_HUMAN
ID   Q6ZND4_HUMAN PRELIMINARY;      PRT;   171 AA.
AC   Q6ZND4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein FLJ16195.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thalamus;
RA   Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
RA   Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA   Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA   Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA   Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA   Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA   Masuho Y., Nagai K., Isogai T.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK131263; BAD18441.1; -; mRNA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   InterPro; IPR011650; M20_dimer.
DR   Pfam; PF07687; M20_dimer; 1.
SQ   SEQUENCE   171 AA;  18880 MW;  20816D6D8F214688 CRC64;

  Query Match           29.1%;  Score 148;  DB 2;  Length 171;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-133;
  Matches  148;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        340 MHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVF 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEKQVTRHLEDVF 60

Qy        400 SKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQ 459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMFQ 120

Qy        460 EIVHKSVVLIPLGAVDDGEHSQNEKINR 487
              |||||||||||||||||||||||||||||
Db        121 EIVHKSVVLIPLGAVDDGEHSQNEKINR 148


RESULT 3
Q5RA69_PONPY
ID   Q5RA69_PONPY PRELIMINARY;      PRT;   464 AA.
AC   Q5RA69;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein DKFZp459C1929.
GN   Name=DKFZp459C1929;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Cortex;
RG   The German cDNA Consortium;
RA   Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA   Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR859150; CAH91341.1; -; mRNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   464 AA;  51970 MW;  7AA5EAF536B0FF3C CRC64;

  Query Match           28.5%;  Score 145;  DB 2;  Length 464;
  Best Local Similarity  100.0%;  Pred. No. 7.2e-130;
  Matches  145;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        106 GQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGAT 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRGAT 121

Qy        166 DNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYI 225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 DNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYI 181

Qy        226 VISDNLWISQRKPAITYGTRGNSYF 250
              |||||||||||||||||||||||||
Db        182 VISDNLWISQRKPAITYGTRGNSYF 206


RESULT 4
Q80XP5_MOUSE
ID   Q80XP5_MOUSE PRELIMINARY;      PRT;   492 AA.
AC   Q80XP5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE   Carnosine dipeptidase 1 (Metallopeptidase M20 family).
GN   Name=Cndp1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC043305; AAH43305.1; -; mRNA.
DR   MEROPS; M20.006; -.
DR   MGI; MGI:2451097; Cndp1.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
SQ   SEQUENCE   492 AA;  55056 MW;  8F5C3AFD859EC804 CRC64;

  Query Match             6.3%;  Score 32;  DB 2;  Length 492;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-21;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        339 LMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV 370
              ||||||||||||||||||||||||||||||||
Db        313 LMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV 344


RESULT 5
Q8BUG2_MOUSE
ID   Q8BUG2_MOUSE PRELIMINARY;      PRT;   492 AA.
AC   Q8BUG2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched
DE   library, clone:D630009N02 product:similar to GLUTAMATE
DE   CARBOXYPEPTIDASE-LIKE PROTEIN 2.
GN   Name=Cndp1; Synonyms=Cn1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Kidney;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
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RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK085308; BAC39417.1; -; mRNA.
DR   MEROPS; M20.006; -.
DR   Ensembl; ENSMUSG00000056162; Mus musculus.
DR   MGI; MGI:2451097; Cndp1.
DR   GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
KW   Carboxypeptidase.
SQ   SEQUENCE   492 AA;  55090 MW;  5A3E3F984CBF4567 CRC64;

  Query Match             6.3%;  Score 32;  DB 2;  Length 492;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-21;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        339 LMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV 370
              ||||||||||||||||||||||||||||||||
Db        313 LMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV 344


RESULT 6
Q66HG3_RAT
ID   Q66HG3_RAT  PRELIMINARY;      PRT;   492 AA.
AC   Q66HG3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Similar to carnosinase 1.
GN   Name=MGC93742;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC081877; AAH81877.1; -; mRNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
SQ   SEQUENCE   492 AA;  54927 MW;  EF8DAE8C15BF06F5 CRC64;

  Query Match             5.9%;  Score 30;  DB 2;  Length 492;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-19;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        341 HLWRYPSLSIHGIEGAFDEPGTKTVIPGRV 370
              ||||||||||||||||||||||||||||||
Db        315 HLWRYPSLSIHGIEGAFDEPGTKTVIPGRV 344


RESULT 7
Q8I1B0_DROWI
ID   Q8I1B0_DROWI PRELIMINARY;      PRT;   357 AA.
AC   Q8I1B0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   CG17337-PA (Fragment).
GN   ORFNames=CG17337;
OS   Drosophila willistoni (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7260;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Tucson 14030-0814.10;
RA   Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
RA   Gnirke A., Mungall C.J., Wang A.M., Kronmiller B., Pacleb J., Park S.,
RA   Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
RA   Celniker S.E.;
RT   "Assessing the impact of comparative genomic sequence data on the
RT   functional annotation of the Drosophila genome.";
RL   Genome Biol. 3:research0086-research0086(2002).
DR   EMBL; AY190950; AAO01061.1; -; Genomic_DNA.
DR   FlyBase; FBgn0064294; Dwil\CG17337.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
FT   NON_TER     357    357
SQ   SEQUENCE   357 AA;  39775 MW;  2016BB8876040141 CRC64;

  Query Match             3.0%;  Score 15;  DB 2;  Length 357;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        343 WRYPSLSIHGIEGAF 357
              |||||||||||||||
Db        316 WRYPSLSIHGIEGAF 330


RESULT 8
Q8I1J9_DROVI
ID   Q8I1J9_DROVI PRELIMINARY;      PRT;   471 AA.
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AC   Q8I1J9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   CG17337.
GN   ORFNames=CG17337;
OS   Drosophila virilis (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7244;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
RA   Gnirke A., Mungall C.J., Wang A.M., Kronmiller B., Pacleb J., Park S.,
RA   Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
RA   Celniker S.E.;
RT   "Assessing the impact of comparative genomic sequence data on the
RT   functional annotation of the Drosophila genome.";
RL   Genome Biol. 3:research0086-research0086(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Pfeiffer B.D., Bergman C.M., George R.A., Mungall C.J., Pacleb J.,
RA   Park S., Wan K.W., Rubin G.M., Celniker S.E.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY186999; AAN87275.1; -; Genomic_DNA.
DR   FlyBase; FBgn0064314; Dvir\CG17337.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
SQ   SEQUENCE   471 AA;  52672 MW;  16837C27B556D9AD CRC64;

  Query Match             3.0%;  Score 15;  DB 2;  Length 471;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        343 WRYPSLSIHGIEGAF 357
              |||||||||||||||
Db        307 WRYPSLSIHGIEGAF 321


RESULT 9
Q6C1A8_YARLI
ID   Q6C1A8_YARLI PRELIMINARY;      PRT;   478 AA.
AC   Q6C1A8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Yarrowia lipolytica chromosome F of strain CLIB99 of Yarrowia
DE   lipolytica.
GN   OrderedLocusNames=YALI0F17842g;
OS   Yarrowia lipolytica (Candida lipolytica).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Dipodascaceae; Yarrowia.
OX   NCBI_TaxID=4952;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15229592; DOI=10.1038/nature02579;
RA   Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA   Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA   Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA   Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA   Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA   Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA   Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA   Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA   Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA   Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA   Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA   Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA   Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA   Wincker P., Souciet J.-L.;
RT   "Genome evolution in yeasts.";
RL   Nature 430:35-44(2004).
DR   EMBL; CR382132; CAG78363.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
KW   Complete proteome.
SQ   SEQUENCE   478 AA;  52510 MW;  995D0F33F5FFCDA2 CRC64;

  Query Match             3.0%;  Score 15;  DB 2;  Length 478;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        343 WRYPSLSIHGIEGAF 357
              |||||||||||||||
Db        311 WRYPSLSIHGIEGAF 325


RESULT 10
Q4WWD5_ASPFU
ID   Q4WWD5_ASPFU PRELIMINARY;      PRT;   478 AA.
AC   Q4WWD5;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Glutamate carboxypeptidase, putative.
GN   ORFNames=Afu3g05450;
OS   Aspergillus fumigatus Af293.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=330879;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Af293;
RA   Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA   Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA   Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
RA   Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA   Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA   Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA   Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA   Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA   Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA   Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA   Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA   Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA   Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA   Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA   Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA   Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA   Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA   White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA   Machida M., Hall N., Barrell B., Denning D.W.;
RT   "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT   Aspergillus fumigatus.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHF01000002; EAL93018.1; -; Genomic_DNA.
KW   Carboxypeptidase.
SQ   SEQUENCE   478 AA;  53015 MW;  62481C384B095CDB CRC64;
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  Query Match             3.0%;  Score 15;  DB 2;  Length 478;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        343 WRYPSLSIHGIEGAF 357
              |||||||||||||||
Db        309 WRYPSLSIHGIEGAF 323


RESULT 11
Q8AWF8_XENLA
ID   Q8AWF8_XENLA PRELIMINARY;      PRT;   489 AA.
AC   Q8AWF8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Glutamate carboxypeptidase (Darmin protein).
GN   Name=Darmin; Synonyms=darmin;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22597554; PubMed=12711541; DOI=10.1016/S1567-133X(03)00011-5;
RA   Pera E.M., Martinez S.L., Flanagan J.J., Brechner M., Wessely O.,
RA   De Robertis E.M.;
RT   "Darmin is a novel secreted protein expressed during endoderm
RT   development in Xenopus.";
RL   Gene Expr. Patterns 3:147-152(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY166869; AAN86572.1; -; mRNA.
DR   EMBL; BC055979; AAH55979.1; -; mRNA.
DR   GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
KW   Carboxypeptidase.
SQ   SEQUENCE   489 AA;  54277 MW;  CB793D2A35537E86 CRC64;

  Query Match             3.0%;  Score 15;  DB 2;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        343 WRYPSLSIHGIEGAF 357
              |||||||||||||||
Db        323 WRYPSLSIHGIEGAF 337


RESULT 12
Q7ZXA6_XENLA
ID   Q7ZXA6_XENLA PRELIMINARY;      PRT;   494 AA.
AC   Q7ZXA6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Darmin protein (Fragment).
GN   Name=darmin;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
```

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DR   EMBL; BC045077; AAH45077.1; -; mRNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   494 AA;  54813 MW;  2E349630FCF08147 CRC64;

  Query Match             3.0%;  Score 15;  DB 2;  Length 494;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        343 WRYPSLSIHGIEGAF 357
              |||||||||||||||
Db        328 WRYPSLSIHGIEGAF 342


RESULT 13
Q801E4_XENLA
ID   Q801E4_XENLA PRELIMINARY;      PRT;   500 AA.
AC   Q801E4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Glutamate carboxypeptidase-like protein 1 (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22480013; PubMed=12591597; DOI=10.1016/S0925-4773(02)00460-4;
RA   Chen Y., Jurgens K., Hollemann T., Claussen M., Ramadori G.,
RA   Pieler T.;
RT   "Cell-autonomous and signal-dependent expression of liver and
RT   intestine marker genes in pluripotent precursor cells from Xenopus
RT   embryos.";
RL   Mech. Dev. 120:277-288(2003).
DR   EMBL; AY188285; AAO31611.1; -; mRNA.
DR   GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
KW   Carboxypeptidase.
FT   NON_TER       1       1
SQ   SEQUENCE   500 AA;  55479 MW;  F2FCB0B3AD4879E4 CRC64;

  Query Match             3.0%;  Score 15;  DB 2;  Length 500;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        343 WRYPSLSIHGIEGAF 357
              |||||||||||||||
Db        334 WRYPSLSIHGIEGAF 348


RESULT 14
Q6PA54_XENLA
ID   Q6PA54_XENLA PRELIMINARY;      PRT;   494 AA.
AC   Q6PA54;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   MGC68563 protein.
GN   Name=MGC68563;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Strausberg R.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC060450; AAH60450.1; -; mRNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
SQ   SEQUENCE   494 AA;  54651 MW;  48D50E78121B7BFD CRC64;

  Query Match             2.6%;  Score 13;  DB 2;  Length 494;
  Best Local Similarity   100.0%;  Pred. No. 0.004;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 DNKGPVLAWINAV 178
              |||||||||||||
Db        141 DNKGPVLAWINAV 153


RESULT 15
Q7ZZU2_OREMO
ID   Q7ZZU2_OREMO PRELIMINARY;      PRT;   184 AA.
AC   Q7ZZU2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE   Glutamate carboxypeptidase-like protein 1 (Fragment).
OS   Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC   Cichlidae; African cichlids; Pseudocrenilabrinae; Tilapiini;
OC   Oreochromis.
OX   NCBI_TaxID=8127;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lo M.J., Chan L.W., Weng C.F.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY260749; AAP22042.1; -; mRNA.
DR   MEROPS; M20.005; -.
DR   GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
KW   Carboxypeptidase.
FT   NON_TER       1      1
FT   NON_TER     184    184
SQ   SEQUENCE   184 AA;  20271 MW;  2F2931433DA71E9A CRC64;

  Query Match             2.2%;  Score 11;  DB 2;  Length 184;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 VIGKFSIRLVP 380
              ||||||||||| 
Db         49 VIGKFSIRLVP 59


RESULT 16
Q4RLC4_TETNG
ID   Q4RLC4_TETNG PRELIMINARY;      PRT;   407 AA.
AC   Q4RLC4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 21 SCAF15022, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00032549001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01015022; CAG10808.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   407 AA;  45539 MW;  4C5BBA5CECC249B4 CRC64;

  Query Match             2.2%;  Score 11;  DB 2;  Length 407;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 VIGKFSIRLVP 380
              ||||||||||| 
Db        269 VIGKFSIRLVP 279


RESULT 17
Q6DH98_BRARE
ID   Q6DH98_BRARE PRELIMINARY;      PRT;   474 AA.
AC   Q6DH98;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Cytosolic nonspecific dipeptidase.
GN   Name=cndp2;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AB; TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AB; TISSUE=Whole body;
RA   Director MGC Project;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC076079; AAH76079.1; -; mRNA.
DR   ZFIN; ZDB-GENE-030131-5499; cndp2.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
SQ   SEQUENCE   474 AA;  53212 MW;  A48D0B1EBEACFB67 CRC64;

  Query Match             2.2%;  Score 11;  DB 2;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        370 VIGKFSIRLVP 380
              ||||||||||
Db        336 VIGKFSIRLVP 346
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RESULT 18
Q6DJK5_XENLA
ID   Q6DJK5_XENLA PRELIMINARY;   PRT;   474 AA.
AC   Q6DJK5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Cndp2-prov protein.
GN   Name=cndp2-prov;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Klein S., Gerhard D.S.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC075171; AAH75171.1; -; mRNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
SQ   SEQUENCE   474 AA; 52840 MW; F97784E8FB36CB78 CRC64;

  Query Match   2.2%; Score 11; DB 2; Length 474;
  Best Local Similarity   100.0%; Pred. No. 0.32;
  Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy        370 VIGKFSIRLVP 380
              ||||||||||
Db        336 VIGKFSIRLVP 346
```

RESULT 19
Q6P358_XENTR
ID   Q6P358_XENTR PRELIMINARY;   PRT;   474 AA.
AC   Q6P358;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC75655.
GN   Name=MGC75655;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC064175; AAH64175.1; -; mRNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   474 AA; 52722 MW; E0D6F40C7EB7E0E3 CRC64;

  Query Match   2.2%; Score 11; DB 2; Length 474;
  Best Local Similarity   100.0%; Pred. No. 0.32;
  Matches   11; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy        370 VIGKFSIRLVP 380
              ||||||||||
Db        336 VIGKFSIRLVP 346
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RESULT 20
Q6TNV3_BRARE

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ID   Q6TNV3_BRARE PRELIMINARY;      PRT;   474 AA.
AC   Q6TNV3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cytosolic nonspecific dipeptidase.
GN   Name=cndp2; Synonyms=CN2;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15520368; DOI=10.1073/pnas.0407241101;
RA   Song H.-D., Sun X.-J., Deng M., Zhang G.-W., Zhou Y., Wu X.-Y.,
RA   Sheng Y., Chen Y., Ruan Z., Jiang C.-L., Fan H.-Y., Zon L.I.,
RA   Kanki J.P., Liu T.X., Look A.T., Chen Z.;
RT   "Hematopoietic gene expression profile in zebrafish kidney marrow.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:16240-16245(2004).
DR   EMBL; AY391414; AAQ91226.1; -; mRNA.
DR   ZFIN; ZDB-GENE-030131-5499; cndp2.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
SQ   SEQUENCE   474 AA;  53134 MW;  5147C209BD4D8AC6 CRC64;

  Query Match             2.2%;  Score 11;  DB 2;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 VIGKFSIRLVP 380
              ||||||||||| 
Db        336 VIGKFSIRLVP 346


RESULT 21
Q7T0R7_XENLA
ID   Q7T0R7_XENLA PRELIMINARY;      PRT;   474 AA.
AC   Q7T0R7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cn2-prov protein.
GN   Name=cn2-prov;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Klein S., Gerhard D.S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056069; AAH56069.1; -; mRNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
SQ   SEQUENCE   474 AA;  52745 MW;  33D9F60F6D375FEF CRC64;

  Query Match             2.2%;  Score 11;  DB 2;  Length 474;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 VIGKFSIRLVP 380
              ||||||||||| 
Db        336 VIGKFSIRLVP 346


RESULT 22
Q5ZLV5_CHICK
ID   Q5ZLV5_CHICK PRELIMINARY;      PRT;   475 AA.
AC   Q5ZLV5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=RCJMB04_419;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CB; TISSUE=Bursa;
RA   Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA   Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA   Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT   "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT   genefunction analysis.";
RL   Genome Biol. 6:R6-R6(2005).
DR   EMBL; AJ719629; CAG31288.1; -; mRNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
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DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   475 AA;  53078 MW;  E7ED4945EB1DD5A5 CRC64;

  Query Match             2.2%;  Score 11;  DB 2;  Length 475;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 VIGKFSIRLVP 380
              ||||||||||| 
Db        336 VIGKFSIRLVP 346


RESULT 23
Q5B7M1_EMENI
ID   Q5B7M1_EMENI PRELIMINARY;      PRT;   477 AA.
AC   Q5B7M1;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=AN3459.2;
OS   Aspergillus nidulans FGSC A4.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=227321;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FGSC A4;
RA   Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA   Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA   Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA   Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA   Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA   Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA   Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA   Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA   Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA   Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA   Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA   Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA   Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA   Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA   Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA   Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA   Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA   Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA   Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA   Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA   Lander E.;
RT   "Genome Sequence of Aspergillus nidulans.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACD01000058; EAA62999.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   477 AA;  52644 MW;  2AA6EFF6EE685831 CRC64;

  Query Match             2.2%;  Score 11;  DB 2;  Length 477;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        346 PSLSIHGIEGA 356
              ||||||||||| 
Db        312 PSLSIHGIEGA 322


RESULT 24
Q9V9H1_DROME
ID   Q9V9H1_DROME PRELIMINARY;      PRT;   478 AA.
AC   Q9V9H1; Q8MT58; Q9V9H2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   CG17337-PA (RE11562p).
GN   ORFNames=CG17337;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
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RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RG   Berkeley Drosophila Genome Project;
RA   Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA   Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA   Yu C., Rubin G.;
RT   "Drosophila melanogaster release 4 sequence.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RG   FlyBase;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- INTERACTION:
CC       Q9V3H2:Rpn11; NbExp=1; IntAct=EBI-144341, EBI-178674;
DR   EMBL; AE003785; AAF57318.2; -; Genomic_DNA.
DR   EMBL; AY118368; AAM48397.1; -; mRNA.
DR   IntAct; Q9V9H1; -.
DR   MEROPS; M20.005; -.
DR   Ensembl; CG17337; Drosophila melanogaster.
DR   FlyBase; FBgn0033035; CG17337.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0046983; F:protein dimerization activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
SQ   SEQUENCE   478 AA;  53163 MW;  D76738B81B7DCA77 CRC64;

  Query Match             2.2%;  Score 11;  DB 2;  Length 478;
  Best Local Similarity   100.0%;  Pred. No. 0.32;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        370 VIGKFSIRLVP 380
              ||||||||||| 
Db        341 VIGKFSIRLVP 351


RESULT 25
Q9ESQ6_MOUSE
ID   Q9ESQ6_MOUSE PRELIMINARY;      PRT;    26 AA.
AC   Q9ESQ6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Prostacyclin synthase (Fragment).
GN   Name=Ptgis;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129SvJ; TISSUE=Spleen;
RA   Ohkawara S., Shimonishi M., Tanabe T., Yokoyama C.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB040750; BAB12574.1; -; Genomic_DNA.
DR   MGI; MGI:1097156; Ptgis.
DR   GO; GO:0005615; C:extracellular space; TAS.
KW   Cyclin.
FT   NON_TER      26     26
SQ   SEQUENCE   26 AA;  2933 MW;  7C110848736AB9E0 CRC64;

  Query Match             2.0%;  Score 10;  DB 2;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 LLAVLLLLLL 21
              ||||||||||
Db          9 LLAVLLLLLL 18


RESULT 26
Q6QMP8_LISMO
ID   Q6QMP8_LISMO PRELIMINARY;      PRT;   156 AA.
AC   Q6QMP8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   DapE (Fragment).
GN   Name=dapE;
OS   Listeria monocytogenes.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1639;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jegot G., Lanotte P., Brun S., Watt S., Quentin R., Mereghetti L.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY533420; AAS22274.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00758; ARGE_DAPE_CPG2_1; UNKNOWN_1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
FT   NON_TER       1      1
FT   NON_TER     156    156
SQ   SEQUENCE   156 AA;  17042 MW;  5ED37075F41238E8 CRC64;

  Query Match             2.0%;  Score 10;  DB 2;  Length 156;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 GKLYGRGATD 166
              ||||||||||
Db         71 GKLYGRGATD 80


RESULT 27
Q6QMP6_LISMO
ID   Q6QMP6_LISMO PRELIMINARY;      PRT;   157 AA.
AC   Q6QMP6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   DapE (Fragment).
GN   Name=dapE;
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```
OS   Listeria monocytogenes.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1639;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jegot G., Lanotte P., Brun S., Watt S., Quentin R., Mereghetti L.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY533422; AAS22276.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00758; ARGE_DAPE_CPG2_1; UNKNOWN_1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
FT   NON_TER       1     1
FT   NON_TER     157   157
SQ   SEQUENCE   157 AA;  17130 MW;  0E0DFBD2E6FE123F CRC64;

  Query Match             2.0%;  Score 10;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 GKLYGRGATD 166
              ||||||||||
Db         71 GKLYGRGATD 80


RESULT 28
Q6QMQ0_LISMO
ID   Q6QMQ0_LISMO PRELIMINARY;      PRT;   157 AA.
AC   Q6QMQ0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   DapE (Fragment).
GN   Name=dapE;
OS   Listeria monocytogenes.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1639;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jegot G., Lanotte P., Brun S., Watt S., Quentin R., Mereghetti L.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY533418; AAS22272.1; -; Genomic_DNA.
DR   EMBL; AY533419; AAS22273.1; -; Genomic_DNA.
DR   EMBL; AY533414; AAS22268.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00758; ARGE_DAPE_CPG2_1; UNKNOWN_1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
FT   NON_TER       1     1
FT   NON_TER     157   157
SQ   SEQUENCE   157 AA;  17143 MW;  FE1ED37075F41238 CRC64;

  Query Match             2.0%;  Score 10;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 GKLYGRGATD 166
              ||||||||||
Db         71 GKLYGRGATD 80


RESULT 29
Q83UJ0_LISMO
ID   Q83UJ0_LISMO PRELIMINARY;      PRT;   159 AA.
AC   Q83UJ0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Succinyldiaminopimelate desuccinylase (Fragment).
GN   Name=dap;
OS   Listeria monocytogenes.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1639;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22461922; PubMed=12574278; DOI=10.1128/JCM.41.2.757-762.2003;
RA   Salcedo C., Arreaza L., Alcala B., de la Fuente L., Vazquez J.A.;
RT   "Development of a multilocus sequence typing method for analysis of
RT   Listeria monocytogenes clones.";
RL   J. Clin. Microbiol. 41:757-762(2003).
DR   EMBL; AY158306; AAO19546.1; -; Genomic_DNA.
DR   EMBL; AY158307; AAO19547.1; -; Genomic_DNA.
DR   EMBL; AY158308; AAO19548.1; -; Genomic_DNA.
DR   EMBL; AY158309; AAO19549.1; -; Genomic_DNA.
DR   EMBL; AY158315; AAO19555.1; -; Genomic_DNA.
DR   EMBL; AY158314; AAO19554.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00758; ARGE_DAPE_CPG2_1; UNKNOWN_1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
FT   NON_TER       1     1
FT   NON_TER     159   159
SQ   SEQUENCE   159 AA;  17248 MW;  44B9F7B64A9B7993 CRC64;

  Query Match             2.0%;  Score 10;  DB 2;  Length 159;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        157 GKLYGRGATD 166
              ||||||||||
Db         64 GKLYGRGATD 73


RESULT 30
Q84GK9_LISMO
ID   Q84GK9_LISMO PRELIMINARY;      PRT;   159 AA.
AC   Q84GK9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Succinyldiaminopimelate desuccinylase (Fragment).
GN   Name=dap;
OS   Listeria monocytogenes.
OC   Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX   NCBI_TaxID=1639;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22461922; PubMed=12574278; DOI=10.1128/JCM.41.2.757-762.2003;
RA   Salcedo C., Arreaza L., Alcala B., de la Fuente L., Vazquez J.A.;
RT   "Development of a multilocus sequence typing method for analysis of
RT   Listeria monocytogenes clones.";
RL   J. Clin. Microbiol. 41:757-762(2003).
DR   EMBL; AY158310; AAO19550.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   PROSITE; PS00758; ARGE_DAPE_CPG2_1; UNKNOWN_1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; 1.
FT   NON_TER       1     1
FT   NON_TER     159   159
SQ   SEQUENCE   159 AA;  17260 MW;  44A3DEB64A9B7993 CRC64;
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Query Match 2.0%; Score 10; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        157 GKLYGRGATD 166
              ||||||||||
Db         64 GKLYGRGATD 73
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Search completed: March 30, 2006, 09:11:52
Job time : 242 secs